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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:01:47 ; Search time 147.75 Seconds  
(without alignments)  
1287.197 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGKKRKRVEISAPNSFHR.....LAKAGPPASIVPLMRQNRTR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3090	100.0	591	10	US-09-291-417-103
2	3090	100.0	591	14	US-10-134-102-4
3	3090	100.0	591	15	US-10-394-322A-48
4	3090	100.0	591	16	US-10-693-367-2
5	3075	99.5	588	14	US-10-134-102-1
6	2073	67.1	398	10	US-09-291-417-30
7	1748	56.6	719	14	US-10-331-095-2
8	1731	56.0	719	14	US-10-331-095-4
9	1731	56.0	719	15	US-10-394-322A-49
10	1502	48.6	292	15	US-10-406-676-5
11	1502	48.6	292	15	US-10-406-676-6
12	1502	48.6	292	15	US-10-406-676-8
13	1502	48.6	292	15	US-10-406-676-9
14	1502	48.6	292	15	US-10-406-676-10
15	1502	48.6	292	15	US-10-406-676-11

16	1502	48.6	293	15	US-10-406-676-4	Sequence 4, Appli
17	1497.5	48.5	639	14	US-10-134-102-6	Sequence 6, Appli
18	1494.5	48.4	635	14	US-10-134-102-2	Sequence 2, Appli
19	1481	47.9	292	15	US-10-406-676-7	Sequence 7, Appli
20	1481	47.9	292	15	US-10-406-676-12	Sequence 12, Appli
21	1473.5	47.7	681	10	US-09-291-417-29	Sequence 29, Appli
22	1470.5	47.6	681	10	US-09-765-815-2	Sequence 2, Appli
23	1421	46.0	292	15	US-10-406-676-15	Sequence 15, Appli
24	1335.5	43.2	641	16	US-10-311-034-15	Sequence 13, Appli
25	1303	42.2	290	15	US-10-406-676-13	Sequence 14, Appli
26	1289	41.7	290	15	US-10-406-676-14	Sequence 16, Appli
27	1289	41.7	290	15	US-10-406-676-16	Sequence 17, Appli
28	1289	41.7	290	15	US-10-406-676-17	Sequence 3, Appli
29	1277	41.3	250	16	US-10-693-367-3	Sequence 18, Appli
30	1213	39.3	290	15	US-10-406-676-18	Sequence 19, Appli
31	1209	39.1	290	15	US-10-406-676-20	Sequence 20, Appli
32	1209	39.1	290	15	US-10-406-676-21	Sequence 21, Appli
33	1147	37.1	292	15	US-10-406-676-21	Sequence 6482, Ap
34	1096.5	35.5	540	15	US-10-369-493-6482	Sequence 6483, Ap
35	1090.5	35.3	542	15	US-10-108-260A-3288	Sequence 3288, App
36	1024.5	33.2	580	12	US-10-267-502-378	Sequence 382, App
37	937.5	30.3	704	12	US-10-267-502-382	Sequence 6, Appli
38	924	29.9	544	12	US-09-967-624-6	Sequence 379, App
39	909	29.4	544	12	US-10-267-502-379	Sequence 6, Appli
40	909	29.4	544	14	US-10-289-161A-6	Sequence 47, Appli
41	909	29.4	544	15	US-10-394-322A-47	Sequence 95, Appli
42	909	29.4	544	10	US-08-291-417-95	Sequence 749, App
43	907	29.4	544	10	US-10-072-012-749	Sequence 4, Appli
44	904	29.3	524	12		
45	904	29.3	524	13	US-10-029-905-4	

## ALIGNMENTS

RESULT 1  
US-09-291-417-103  
; Sequence 103, Application US/09291417A  
; Publication No. US20030050230A1  
; GENERAL INFORMATION:  
; APPLICANT: FLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 240/300  
; CURRENT APPLICATION NUMBER: US/09/291,417A  
; CURRENT FILING DATE: 1999-04-13  
; EARLIER APPLICATION NUMBER: US 60/081,784  
; EARLIER FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 103  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Full Length Mammalian (Human) PAK5hu  
US-09-291-417-103

Query Match 100.0%; Score 3090; DB 10; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.4e-167;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFGKKRKRVEISAPNSFHRVHTGFDQHQKFTGLPRQWQSLIESARRPKPLVDPA	60
DB	1	MFGKKRKRVEISAPNSFHRVHTGFDQHQKFTGLPRQWQSLIESARRPKPLVDPA	60
QY	61	SIQGPAPKTIYRSGKAGKDGALTLLDEFENWSTRTNSLRDPPPPARARQENGMP	120
DB	61	SIQGPAPKTIYRSGKAGKDGALTLLDEFENWSTRTNSLRDPPPPARARQENGMP	120
QY	121	PATTARGGPGKAGRGFRAGHSEAGGSGDRRRAGPEKRRPKSSREGSGGPQESS	180
DB	121	PATTARGGPGKAGRGFRAGHSEAGGSGDRRRAGPEKRRPKSSREGSGGPQESS	180

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QY 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPGRGAQGEHDVAPNGSPSAGGLAIP 240
Db 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPGRGAQGEHDVAPNGSPSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPSPQREPQVRS 300
Db 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPSPQREPQVRS 300
QY 301 HEGFRAALQVLDGDPSPSYLDNFIKIGEGSTGIVCIATVRSCKLVAVKMDLRKQORR 360
Db 301 HEGFRAALQVLDGDPSPSYLDNFIKIGEGSTGIVCIATVRSCKLVAVKMDLRKQORR 360
QY 361 ELLEFNEVIMRDYQHENVVEMYSYLVGDDELWVMEFEGGALTDIVTHRMNEEQIAAV 420
Db 361 ELLEFNEVIMRDYQHENVVEMYSYLVGDDELWVMEFEGGALTDIVTHRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480
Db 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDEGPPYFNEPPLKAMKMIKMDLRKQORR 540
Db 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDEGPPYFNEPPLKAMKMIKMDLRKQORR 540
QY 541 VSPSLKGFDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591
Db 541 VSPSLKGFDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591

RESULT 2
US-10-134-102-4
; Sequence 4, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Melnick, Michael B.
; APPLICANT: Moritz, Albrecht
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; CURRENT FILING DATE: 2002-04-29
; PRIOR FILING DATE: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR FILING DATE: 60/173,939
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-4

Query Match 100.0%; Score 3090; DB 14; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.4e-167;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKVEISAPSNFEHRVHTGFDQHQKFTGLPRQWQSLIESARRPKPLVDPAIT 60
Db 1 MFGKRRKVEISAPSNFEHRVHTGFDQHQKFTGLPRQWQSLIESARRPKPLVDPAIT 60
QY 61 SIOPGAPKTIVRGSKGAKDGNLTLLDEFENMVSITRNSLRDSDPPPPARQNGMPPEE 120
Db 61 SIOPGAPKTIVRGSKGAKDGNLTLLDEFENMVSITRNSLRDSDPPPPARQNGMPPEE 120
QY 121 PATTARGGPKAGSRGFRAGHSEAGGSGGRRRAGPEKPKSSREGSGGQESRRDKRPL 180
Db 121 PATTARGGPKAGSRGFRAGHSEAGGSGGRRRAGPEKPKSSREGSGGQESRRDKRPL 180
QY 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPGRGAQGEHDVAPNGSPSAGGLAIP 240
Db 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPGRGAQGEHDVAPNGSPSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPSPQREPQVRS 300
Db 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPSPQREPQVRS 300
QY 301 HEGFRAALQVLDGDPSPSYLDNFIKIGEGSTGIVCIATVRSCKLVAVKMDLRKQORR 360
Db 301 HEGFRAALQVLDGDPSPSYLDNFIKIGEGSTGIVCIATVRSCKLVAVKMDLRKQORR 360
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QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPSPQREPQVRS 300
Db 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPSPQREPQVRS 300
QY 301 HEGFRAALQVLDGDPSPSYLDNFIKIGEGSTGIVCIATVRSCKLVAVKMDLRKQORR 360
Db 301 HEGFRAALQVLDGDPSPSYLDNFIKIGEGSTGIVCIATVRSCKLVAVKMDLRKQORR 360
QY 361 ELLEFNEVIMRDYQHENVVEMYSYLVGDDELWVMEFEGGALTDIVTHRMNEEQIAAV 420
Db 361 ELLEFNEVIMRDYQHENVVEMYSYLVGDDELWVMEFEGGALTDIVTHRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480
Db 421 CLAVLQALSVLHAQGVVHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDEGPPYFNEPPLKAMKMIKMDLRKQORR 540
Db 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDEGPPYFNEPPLKAMKMIKMDLRKQORR 540
QY 541 VSPSLKGFDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591
Db 541 VSPSLKGFDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMQNRTR 591

RESULT 3
US-10-394-322A-48
; Sequence 48, Application US/10394322A
; Publication No. US2003023291A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-48

Query Match 100.0%; Score 3090; DB 15; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.4e-167;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKVEISAPSNFEHRVHTGFDQHQKFTGLPRQWQSLIESARRPKPLVDPAIT 60
Db 1 MFGKRRKVEISAPSNFEHRVHTGFDQHQKFTGLPRQWQSLIESARRPKPLVDPAIT 60
QY 61 SIOPGAPKTIVRGSKGAKDGNLTLLDEFENMVSITRNSLRDSDPPPPARQNGMPPEE 120
Db 61 SIOPGAPKTIVRGSKGAKDGNLTLLDEFENMVSITRNSLRDSDPPPPARQNGMPPEE 120
QY 121 PATTARGGPKAGSRGFRAGHSEAGGSGGRRRAGPEKPKSSREGSGGQESRRDKRPL 180
Db 121 PATTARGGPKAGSRGFRAGHSEAGGSGGRRRAGPEKPKSSREGSGGQESRRDKRPL 180
QY 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPGRGAQGEHDVAPNGSPSAGGLAIP 240
Db 181 SGPVGTGPAGLASGAKLAAGRPNTYPRADTDHPGRGAQGEHDVAPNGSPSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPSPQREPQVRS 300
Db 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPSPQREPQVRS 300
QY 301 HEGFRAALQVLDGDPSPSYLDNFIKIGEGSTGIVCIATVRSCKLVAVKMDLRKQORR 360
Db 301 HEGFRAALQVLDGDPSPSYLDNFIKIGEGSTGIVCIATVRSCKLVAVKMDLRKQORR 360
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301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSEGLVAVKMDLRKQORR 360  
QY 361 ELLFNEVVMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420  
Db 361 ELLFNEVVMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420  
QY 421 CLAVLQALSVLHAOGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480  
Db 421 CLAVLQALSVLHAOGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480  
QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVMDGEPYFNEPPLKAMKMIKMDNLPRLKNIHK 540  
Db 481 WMAPELISRLPYGPEVDIWSLGIWVEMVMDGEPYFNEPPLKAMKMIKMDNLPRLKNIHK 540  
QY 541 VSPSLKGFLLRDLVDRPAQRATAAELLKHPLAKAGPPASIVPLMRQNRTR 591  
Db 541 VSPSLKGFLLRDLVDRPAQRATAAELLKHPLAKAGPPASIVPLMRQNRTR 591  
RESULT 4  
US-10-693-367-2  
; Sequence 2, Application US/10693367  
; Publication No. US2004009192A1  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE  
; FILE REFERENCE: 575/55311-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/693,367  
; CURRENT FILING DATE: 2003-10-24  
; PRIOR APPLICATION NUMBER: US/09/718,032  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: PCT/US99/11341  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 09/082,737  
; PRIOR FILING DATE: 1998-05-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: human  
US-10-693-367-2  
Query Match 100.0%; Score 3090; DB 16; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.4e-167;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKRVISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIEESARRPKPLVDPACIT 60  
Db 1 MFGKRRKRVISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIEESARRPKPLVDPACIT 60  
QY 61 SIQPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120  
Db 61 SIQPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120  
QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKPKSRREGSGGPPQESSRDKRPL 180  
Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKPKSRREGSGGPPQESSRDKRPL 180  
QY 181 SGPDVGTTPQAGLAGAKLAAGRPNTYPRADTDHPSGAQGEHVDVAPNGPSAGGLAIP 240  
Db 181 SGPDVGTTPQAGLAGAKLAAGRPNTYPRADTDHPSGAQGEHVDVAPNGPSAGGLAIP 240  
QY 241 QSSSSSRPPPTARCAPSPGVLGPHASEPQLAPACTPAAPVAPGPPGPRSPQREPORVS 300  
Db 241 QSSSSSRPPPTARCAPSPGVLGPHASEPQLAPACTPAAPVAPGPPGPRSPQREPORVS 300  
QY 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSEGLVAVKMDLRKQORR 360  
Db 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSEGLVAVKMDLRKQORR 360  
QY 361 ELLFNEVVMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420  
Db 361 ELLFNEVVMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420

361 ELLFNEVVMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420  
QY 421 CLAVLQALSVLHAOGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480  
Db 421 CLAVLQALSVLHAOGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480  
QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVMDGEPYFNEPPLKAMKMIKMDNLPRLKNIHK 540  
Db 481 WMAPELISRLPYGPEVDIWSLGIWVEMVMDGEPYFNEPPLKAMKMIKMDNLPRLKNIHK 540  
QY 541 VSPSLKGFLLRDLVDRPAQRATAAELLKHPLAKAGPPASIVPLMRQNRTR 591  
Db 541 VSPSLKGFLLRDLVDRPAQRATAAELLKHPLAKAGPPASIVPLMRQNRTR 591  
RESULT 5  
US-10-134-102-1  
; Sequence 1, Application US/10134102  
; Publication No. US20030186254A1  
; GENERAL INFORMATION:  
; APPLICANT: Moritz, Michael B.  
; APPLICANT: Comb, Michael J.  
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its  
; TITLE OF INVENTION: binding partners and methods of identifying modulators thereof.  
; FILE REFERENCE: CST-176 CIP  
; CURRENT APPLICATION NUMBER: US/10/134,102  
; CURRENT FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: 09/750,457  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: 60/173,939  
; PRIOR FILING DATE: 1999-12-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-134-102-1  
Query Match 99.5%; Score 3075; DB 14; Length 588;  
Best Local Similarity 100.0%; Pred. No. 9.8e-167;  
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKRRKRVISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIEESARRPKPLVDPACIT 60  
Db 1 MFGKRRKRVISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIEESARRPKPLVDPACIT 60  
QY 61 SIQPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120  
Db 61 SIQPGAPKTIVRGSKGADGALTLLDDEFENMVSRTNSLRDSDPPPPARARQENGMPPEE 120  
QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKPKSRREGSGGPPQESSRDKRPL 180  
Db 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKPKSRREGSGGPPQESSRDKRPL 180  
QY 181 SGPDVGTTPQAGLAGAKLAAGRPNTYPRADTDHPSGAQGEHVDVAPNGPSAGGLAIP 240  
Db 181 SGPDVGTTPQAGLAGAKLAAGRPNTYPRADTDHPSGAQGEHVDVAPNGPSAGGLAIP 240  
QY 241 QSSSSSRPPPTARCAPSPGVLGPHASEPQLAPACTPAAPVAPGPPGPRSPQREPORVS 300  
Db 241 QSSSSSRPPPTARCAPSPGVLGPHASEPQLAPACTPAAPVAPGPPGPRSPQREPORVS 300  
QY 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSEGLVAVKMDLRKQORR 360  
Db 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSSEGLVAVKMDLRKQORR 360  
QY 361 ELLFNEVVMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420  
Db 361 ELLFNEVVMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420

QY 421 CLAVLQALSVLHAQVTHRDIKSDSILLTHDGRVKLSDFGFCQAVSKVPRKSLVGTPT 480  
Db 421 CLAVLQALSVLHAQVTHRDIKSDSILLTHDGRVKLSDFGFCQAVSKVPRKSLVGTPT 480  
QY 481 WMAPELISRLPYGPEVDIWSIGIMVIEWVDGEPYFNEPPLKAMKMRDNLPPRLKNLHK 540  
Db 481 WMAPELISRLPYGPEVDIWSIGIMVIEWVDGEPYFNEPPLKAMKMRDNLPPRLKNLHK 540  
QY 541 VSPSLKGFDRLLVRDPAQRATAELLKHPFLAKAGPPASIVPLMRQN 588  
Db 541 VSPSLKGFDRLLVRDPAQRATAELLKHPFLAKAGPPASIVPLMRQN 588

## RESULT 6

US-09-291-417-30  
; Sequence 30, Application US/09291417A  
; Publication No. US20030050230A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 240/300  
; CURRENT APPLICATION NUMBER: US/09/291,417A  
; EARLIER FILING DATE: 1999-04-13  
; EARLIER APPLICATION NUMBER: US 60/081,784  
; EARLIER FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 30  
; LENGTH: 398  
; TYPE: PRT  
; ORGANISM: Mammalian (Human) PAK5  
US-09-291-417-30

Query Match 67.1%; Score 2073; DB 10; Length 398;  
Best Local Similarity 100.0%; Pred. No. 5,3e-110;  
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAAGRPTNTYPRADTDHPSGAQGEPHDVAPNGSPSAGGLAIPQSSSSSRPPTRA 253  
Db 1 ASGAKLAAGRPTNTYPRADTDHPSGAQGEPHDVAPNGSPSAGGLAIPQSSSSSRPPTRA 60  
QY 254 RGAPSPGVLGPHASEPQLAPACTPAAPAVPGPGRSPQRPQVSHQFRAALQLVVD 313  
Db 61 RGAPSPGVLGPHASEPQLAPACTPAAPAVPGPGRSPQRPQVSHQFRAALQLVVD 120  
QY 314 PGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLAVKMDLRKQORRELLFNEVIMRDY 373  
Db 121 PGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLAVKMDLRKQORRELLFNEVIMRDY 180  
QY 374 QHENNVEMYNLYVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHA 433  
Db 181 QHENNVEMYNLYVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHA 240  
QY 434 QGVTHRDIKSDSILLTHDGRVKLSDFGFCQAVSKVPRKSLVGTPTWMAPELISRLPYG 493  
Db 241 QGVTHRDIKSDSILLTHDGRVKLSDFGFCQAVSKVPRKSLVGTPTWMAPELISRLPYG 300  
QY 494 PEVDIWSIGIMVIEWVDGEPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFDRLL 553  
Db 301 PEVDIWSIGIMVIEWVDGEPYFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFDRLL 360  
QY 554 VRDPAQRATAELLKHPFLAKAGPPASIVPLMRQNRT 591  
Db 361 VRDPAQRATAELLKHPFLAKAGPPASIVPLMRQNRT 398

## RESULT 7

US-10-331-095-2  
; Sequence 2, Application US/10331095  
; Publication No. US20030124107A1  
; GENERAL INFORMATION:

; APPLICANT: Columbia University  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAK5-Related Compositions and Methods  
; FILE REFERENCE: 0575/64083-A  
; CURRENT APPLICATION NUMBER: US/10/331,095  
; CURRENT FILING DATE: 2002-12-27  
; PRIOR APPLICATION NUMBER: 60/343,972  
; PRIOR FILING DATE: 2001-12-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: mouse  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: mouse PAK5  
US-10-331-095-2

Query Match 56.6%; Score 1748; DB 14; Length 719;  
Best Local Similarity 52.9%; Pred. No. 2.9e-91;  
Matches 385; Conservative 65; Mismatches 128; Indels 150; Gaps 16;  
QY 1 MFGKRRKRVETISAPSNFEHRVHTGPDQHQKFTGLPRQWOSLIEGARRPKPLVDACIT 60  
Db 1 MFGKRRKRVETISAPSNFEHRVHTGPDQHQKFTGLPRQWOSLIEGARRPKPLVDACIT 60  
QY 61 STOPGAPKTIIVRGSKGAKGALTLTLDPEFNMSVTRNSLRDSDPPPP---ARAR----- 112  
Db 61 PIQLAPMKTIIVRGSKSKETSLELDFDNISVTRNSLRKESPTTPQGAASRIQGH 120  
QY 113 QENGM-----PEEPATTARGGPGKAGSGRGA-----CH----- 141  
Db 121 EENGFTTFOYSSESDDTADYITEKVRDRSLYGGDLDLYKSSHAQKQNGHMKMGDA 180  
QY 142 -----SEAGGSGDRRA----- 154  
Db 181 YYPEMKSLKTLDLAGFPVDYVHTLDSLRSSEYGLDRWDYQRASSSSPLDYSQLTFSRTA 240  
QY 155 -----GP-----EKRPKSREGSGGQESRDRKPLSGPDVGTPT-QPA 191  
Db 241 GTSRCSKESLAYSESDWGFSLDDYDRRPKSSYLHOTSQPAMR-QRSKSGSLQEPMMFF 299  
QY 192 GLASGAKLAAGRPTNTY-----PRADTDH-----PSRGAQGEPHDVAPNGP 232  
Db 300 GASAFKTHPQGHVSNSTYPRLSEPTMCPKVDYDRAQWVFPPLSGS-----DTYPRGP 354  
QY 233 SAGGLAIPQS-----SSSSSRPPTRARGA-----PSGVLGPHASEPQLAPACTPAAP 281  
Db 355 T-----KLPSQSKAGYSSGSHQYPSGYHKASLYHHPSLQTSQYISTASYL-SSLSISS 409  
QY 282 AVPGPPGRSPQRPQVSHQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVR 341  
Db 410 TYPSPSSGSSDQQFSPRSVSHQFRAALQLVVPSPGDPREYLDNFIKIGEGSTGIVCIATEK 469  
QY 342 SSGKLAVKMDLRKQORRELLFNEVIMRDYQHENNVEMYNLYVGDELWVWMEFLEGG 401  
Db 470 HTGQVAVKMDLRKQORRELLFNEVIMRDYHNDNVVDNINSYLVGDELWVWMEFLEGG 529  
QY 402 ALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQVTHRDIKSDSILLTHDGRVKLSDFG 461  
Db 530 ALTDIVTHTRMNEEQIATVCLSVLKALSYLHNOQVTHRDIKSDSILLTSDGRKLSDFG 589  
QY 462 CAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSIGIMVIEWVDGEPYFNEPPL 521  
Db 590 CAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSIGIMVIEWVDGEPYFNEPPL 649  
QY 522 KAMKMRDNLPPRLKNLHKVSPSLKGFDRLLVRDPAQRATAELLKHPFLAKAGPPASI 581  
Db 650 QAMRIRDSLPVRKDLHKVSSMLRGLDMLVREPSQRATAQELLGHPFLKAGPPSCI 709  
QY 582 VPLMRQN 589



Db 710 VPLMRQYR 717

RESULT 8

US-10-331-095-4

; Sequence 4, Application US/10331095

; Publication No. US20030124107A1

; GENERAL INFORMATION:

; APPLICANT: Columbia University

; APPLICANT: Minden, Audrey

; TITLE OF INVENTION: PAK5-Related Compositions and Methods

; FILE REFERENCE: 0575/64083-A

; CURRENT APPLICATION NUMBER: US/10/331,095

; CURRENT FILING DATE: 2002-12-27

; PRIOR APPLICATION NUMBER: 60/343,972

; PRIOR FILING DATE: 2001-12-28

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 719

; TYPE: PRT

; ORGANISM: human

; FEATURE:

; NAME/KEY: MISC\_FEATURE

; OTHER INFORMATION: Human PAK5

US-10-331-095-4

Query Match 56.0%; Score 1731; DB 14; Length 719;

Best Local Similarity 52.4%; Pred. No. 2.6e-90;

Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGRKRRVEISAPSNFHRVHTGFPQHQKFTGLPRQWSLIEESARRPKPLVDPACT 60

Db 1 MFGRKRRVEISAPSNFHRVHTGFPQHQKFTGLPRQWSLIEESARRPKPLVDPACT 60

QY 61 SIOPGAPKTIVRGSKGAKGALTLLEDEFENMSVTRSNLRRDSDPPPPARA-----R 112

Db 61 SIOPGAPKTIVRGSKGAKGALTLLEDEFENMSVTRSNLRRDSDPPPPARA-----R 112

QY 113 QENGM-----PREPATT-----RG-----PGKA 132

Db 113 QENGM-----PREPATT-----RG-----PGKA 132

QY 121 EENGFTIFSQSSSEDTADYTKYREKSLYGDLDPPYVRGSHAAKQNGHVMKMGHEA 180

Db 121 EENGFTIFSQSSSEDTADYTKYREKSLYGDLDPPYVRGSHAAKQNGHVMKMGHEA 180

QY 133 -----GSRGRFAGH-----SEAG 145

Db 133 -----GSRGRFAGH-----SEAG 145

QY 181 YYSEVKPLKSDFAFADYHSHLDSLSPSEYSDLKWEYQORASSSSPLDYSFOFTPERTA 240

Db 181 YYSEVKPLKSDFAFADYHSHLDSLSPSEYSDLKWEYQORASSSSPLDYSFOFTPERTA 240

QY 146 GSGDRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTGTP-QPA 191

Db 146 GSGDRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTGTP-QPA 191

QY 241 GTSGCKESLAYSESEWGPSLDDYDRPKSYLNOTSPQTM-RQSRSGSLQEPMPWF 299

Db 241 GTSGCKESLAYSESEWGPSLDDYDRPKSYLNOTSPQTM-RQSRSGSLQEPMPWF 299

QY 192 GLASGAKLAAGRPNNTY-----PRADTDH-----PSRGAQGEPHVAVNGP 232

Db 192 GLASGAKLAAGRPNNTY-----PRADTDH-----PSRGAQGEPHVAVNGP 232

QY 300 GASAFKTHPQHSYNSYTPRLSEPTWCIPKVDYDRAQMVLSPLSGS-----DTYPRGP 354

Db 300 GASAFKTHPQHSYNSYTPRLSEPTWCIPKVDYDRAQMVLSPLSGS-----DTYPRGP 354

QY 233 SAGGLAIPOS-----SSSSSRPPTARGAPSPVILGPHASEPOLAPACTP----- 278

Db 233 SAGGLAIPOS-----SSSSSRPPTARGAPSPVILGPHASEPOLAPACTP----- 278

QY 355 A-----KLPSQSKSGYSSSHQPSGYHKA-----TLYHHPFSLOQSSQVISTASYLSLSL 406

Db 355 A-----KLPSQSKSGYSSSHQPSGYHKA-----TLYHHPFSLOQSSQVISTASYLSLSL 406

QY 279 AAPAVPPGPRSPQREPVSHQFRAALQLVVDGDPGRSYLDFNFIKIGSGTGIVCIA 338

Db 279 AAPAVPPGPRSPQREPVSHQFRAALQLVVDGDPGRSYLDFNFIKIGSGTGIVCIA 338

QY 407 SSSTYPSPSGSSDQPPSRVSHQFRAALQLVVDGDPGRSYLDFNFIKIGSGTGIVCIA 466

Db 407 SSSTYPSPSGSSDQPPSRVSHQFRAALQLVVDGDPGRSYLDFNFIKIGSGTGIVCIA 466

QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSYLVDGLVWVMEFL 398

Db 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSYLVDGLVWVMEFL 398

QY 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSYLVDGLVWVMEFL 526

Db 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSYLVDGLVWVMEFL 526

QY 399 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 458

Db 399 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 458

QY 527 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 586

Db 527 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 586

QY 459 GFCAQVSKVEPKKSLVGTPTWMAPEVLSRLPYGTEVDIWSLGIWMIEMIDGPPYPNE 518

Db 459 GFCAQVSKVEPKKSLVGTPTWMAPEVLSRLPYGTEVDIWSLGIWMIEMIDGPPYPNE 518

Db 587 GFCAQVSKVEPKKSLVGTPTWMAPEVLSRLPYGTEVDIWSLGIWMIEMIDGPPYPNE 646

QY 519 PPLKAMKWRDNLPPRLKHLKHSVSLKGLDFDRLLVRDPAQATAAEALLKHPFLAKAGPP 578

Db 647 PPLQAMRRIRDSLPVRVDLHKVSVLRGFLDMLVREPSQRATQAQELLGHPFLKAGPP 706

QY 579 ASIIVPLMRQNR 589

Db 707 SCIVPLMRQYR 717

RESULT 9

US-10-394-322A-49

; Sequence 49, Application US/10394322A

; Publication No. US20030232391A1

; GENERAL INFORMATION:

; APPLICANT: SUNESIS PHARMACEUTICALS, INC.

; APPLICANT: Prescott, John C.

; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS

; FILE REFERENCE: 39750-0006 US

; CURRENT APPLICATION NUMBER: US/10/394,322A

; CURRENT FILING DATE: 2003-03-20

; PRIOR APPLICATION NUMBER: US 60/366,892

; PRIOR FILING DATE: 2002-03-21

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49

; LENGTH: 719

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-394-322A-49

Query Match 56.0%; Score 1731; DB 15; Length 719;

Best Local Similarity 52.4%; Pred. No. 2.6e-90;

Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGRKRRVEISAPSNFHRVHTGFPQHQKFTGLPRQWSLIEESARRPKPLVDPACT 60

Db 1 MFGRKRRVEISAPSNFHRVHTGFPQHQKFTGLPRQWSLIEESARRPKPLVDPACT 60

QY 61 SIOPGAPKTIVRGSKGAKGALTLLEDEFENMSVTRSNLRRDSDPPPPARA-----R 112

Db 61 SIOPGAPKTIVRGSKGAKGALTLLEDEFENMSVTRSNLRRDSDPPPPARA-----R 112

QY 113 QENGM-----PREPATT-----RG-----PGKA 132

Db 113 QENGM-----PREPATT-----RG-----PGKA 132

QY 121 EENGFTIFSQSSSEDTADYTKYREKSLYGDLDPPYVRGSHAAKQNGHVMKMGHEA 180

Db 121 EENGFTIFSQSSSEDTADYTKYREKSLYGDLDPPYVRGSHAAKQNGHVMKMGHEA 180

QY 133 -----GSRGRFAGH-----SEAG 145

Db 133 -----GSRGRFAGH-----SEAG 145

QY 181 YYSEVKPLKSDFAFADYHSHLDSLSPSEYSDLKWEYQORASSSSPLDYSFOFTPERTA 240

Db 181 YYSEVKPLKSDFAFADYHSHLDSLSPSEYSDLKWEYQORASSSSPLDYSFOFTPERTA 240

QY 146 GSGDRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTGTP-QPA 191

Db 146 GSGDRRA-----GP-----EKRPKSSREGSGGPOESSRDKRPLSGPDVGTGTP-QPA 191

QY 241 GTSGCKESLAYSESEWGPSLDDYDRPKSYLNOTSPQTM-RQSRSGSLQEPMPWF 299

Db 241 GTSGCKESLAYSESEWGPSLDDYDRPKSYLNOTSPQTM-RQSRSGSLQEPMPWF 299

QY 192 GLASGAKLAAGRPNNTY-----PRADTDH-----PSRGAQGEPHVAVNGP 232

Db 192 GLASGAKLAAGRPNNTY-----PRADTDH-----PSRGAQGEPHVAVNGP 232

QY 300 GASAFKTHPQHSYNSYTPRLSEPTWCIPKVDYDRAQMVLSPLSGS-----DTYPRGP 354

Db 300 GASAFKTHPQHSYNSYTPRLSEPTWCIPKVDYDRAQMVLSPLSGS-----DTYPRGP 354

QY 233 SAGGLAIPOS-----SSSSSRPPTARGAPSPVILGPHASEPOLAPACTP----- 278

Db 233 SAGGLAIPOS-----SSSSSRPPTARGAPSPVILGPHASEPOLAPACTP----- 278

QY 355 A-----KLPSQSKSGYSSSHQPSGYHKA-----TLYHHPFSLOQSSQVISTASYLSLSL 406

Db 355 A-----KLPSQSKSGYSSSHQPSGYHKA-----TLYHHPFSLOQSSQVISTASYLSLSL 406

QY 279 AAPAVPPGPRSPQREPVSHQFRAALQLVVDGDPGRSYLDFNFIKIGSGTGIVCIA 338

Db 279 AAPAVPPGPRSPQREPVSHQFRAALQLVVDGDPGRSYLDFNFIKIGSGTGIVCIA 338

QY 407 SSSTYPSPSGSSDQPPSRVSHQFRAALQLVVDGDPGRSYLDFNFIKIGSGTGIVCIA 466

Db 407 SSSTYPSPSGSSDQPPSRVSHQFRAALQLVVDGDPGRSYLDFNFIKIGSGTGIVCIA 466

QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSYLVDGLVWVMEFL 398

Db 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSYLVDGLVWVMEFL 398

QY 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSYLVDGLVWVMEFL 526

Db 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVVMYNSYLVDGLVWVMEFL 526

QY 399 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 458

Db 399 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 458

QY 527 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 586

Db 527 EGGALTDIVTHTRMNEEQIAAACLAVLOALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD 586

QY 459 GFCAQVSKVEPKKSLVGTPTWMAPEVLSRLPYGTEVDIWSLGIWMIEMIDGPPYPNE 518

Db 459 GFCAQVSKVEPKKSLVGTPTWMAPEVLSRLPYGTEVDIWSLGIWMIEMIDGPPYPNE 518

Db 527 EGGALTDIVTHRMNEQIATVLSVLRALSYLHQGVHRIKSDSILLTSDGRKILSD 586  
Qy 459 FGCAQVSKEVPRKSLVGTGPPYMAPELISRLPYGPEVDIWSLGIWVIMVMDGPPYFNE 518  
Db 587 FGCAQVSKEVPRKSLVGTGPPYMAPEVISELPGTGEVDIWSLGIWVIMVMDGPPYFNE 646  
Qy 519 PPLKAMKMIENDLPPRLKNLHKVSPSLKGFLLRLVRDPAQATAAELLKHPFLAKAGPP 578  
Db 647 PPLQAMRRIRDSLPPRVKDLHKVSSVLRGFLDMLVREPSQATAQELLGHFFLKLAGPP 706  
Qy 579 ASIVPLMRQNR 589  
Db 707 SCIVPLMRQYR 717

## RESULT 10

US-10-406-676-5

; Sequence 5, Application US/10406676

; Publication No. US20030229453A1

; GENERAL INFORMATION:

; APPLICANT: Structural Genomix, Inc.

; APPLICANT: Antonysam, Stephen

; APPLICANT: Feil, Ingeborg

; APPLICANT: Buchanan, Sean

; APPLICANT: Post, Kai W.

; APPLICANT: Liu, Yi

; APPLICANT: Lorber, David

; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE

; FILE OF INVENTION: PAK4KD

; FILE REFERENCE: 524982002300

; CURRENT APPLICATION NUMBER: US/10/406,676

; PRIOR FILING DATE: 2003-04-02

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/430,567

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 292

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-406-676-5

## Query Match

Best Local Similarity 48.6%; Score 1502; DB 15; Length 292;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 300 SHEQFRAALQLVDPDPRSILDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQOR 359  
Db 1 SHEQFRAALQLVDPDPRSILDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQOR 60  
Qy 360 RELFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAA 419  
Db 61 RELFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAA 120  
Qy 420 VCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKEVPRKSLVGTG 479  
Db 121 VCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKEVPRKSLVGTG 180  
Qy 480 YWMAPELISRLPYGPEVDIWSLGIWVIMVMDGPPYFNEPPLKAMKMIENDLPPRLKNLH 539  
Db 181 YWMAPELISRLPYGPEVDIWSLGIWVIMVMDGPPYFNEPPLKAMKMIENDLPPRLKNLH 240  
Qy 540 KVSPLKGFLLRLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
Db 241 KVSPLKGFLLRLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292

## RESULT 11

US-10-406-676-6

; Sequence 6, Application US/10406676

; Publication No. US20030229453A1  
; GENERAL INFORMATION:  
; APPLICANT: Structural Genomix, Inc.  
; APPLICANT: Antonysam, Stephen  
; APPLICANT: Feil, Ingeborg  
; APPLICANT: Buchanan, Sean  
; APPLICANT: Post, Kai W.  
; APPLICANT: Liu, Yi  
; APPLICANT: Lorber, David  
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE  
; FILE OF INVENTION: PAK4KD  
; FILE REFERENCE: 524982002300  
; CURRENT APPLICATION NUMBER: US/10/406,676  
; CURRENT FILING DATE: 2003-04-02  
; PRIOR APPLICATION NUMBER: 60/371,018  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/430,567  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 292  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-406-676-6

## Query Match

Best Local Similarity 48.6%; Score 1502; DB 15; Length 292;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 300 SHEQFRAALQLVDPDPRSILDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQOR 359  
Db 1 SHEQFRAALQLVDPDPRSILDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQOR 60  
Qy 360 RELFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAA 419  
Db 61 RELFNEVIMRDYQHENVVEMYSYLVGDELWVWMEFLEGALTDIVTHRMNEEQIAA 120  
Qy 420 VCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKEVPRKSLVGTG 479  
Db 121 VCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKEVPRKSLVGTG 180  
Qy 480 YWMAPELISRLPYGPEVDIWSLGIWVIMVMDGPPYFNEPPLKAMKMIENDLPPRLKNLH 539  
Db 181 YWMAPELISRLPYGPEVDIWSLGIWVIMVMDGPPYFNEPPLKAMKMIENDLPPRLKNLH 240  
Qy 540 KVSPLKGFLLRLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
Db 241 KVSPLKGFLLRLVRDPAQATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292

## RESULT 12

US-10-406-676-8

; Sequence 8, Application US/10406676

; Publication No. US20030229453A1

; GENERAL INFORMATION:

; APPLICANT: Structural Genomix, Inc.

; APPLICANT: Antonysam, Stephen

; APPLICANT: Feil, Ingeborg

; APPLICANT: Buchanan, Sean

; APPLICANT: Post, Kai W.

; APPLICANT: Liu, Yi

; APPLICANT: Lorber, David

; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE

; FILE OF INVENTION: PAK4KD

; FILE REFERENCE: 524982002300

; CURRENT APPLICATION NUMBER: US/10/406,676

; PRIOR FILING DATE: 2003-04-02

; PRIOR APPLICATION NUMBER: 60/371,018

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/430,567

; PRIOR FILING DATE: 2002-12-02

; NUMBER OF SEQ ID NOS: 21

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-8

Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 359
DB 1 SHEQFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 60

QY 360 RELLEFNEVIMRDYQHENVVEMVNSYLVDGLWVWMEFLEGGALTDIVTHTRMNEEQIAA 419
DB 61 RELLEFNEVIMRDYQHENVVEMVNSYLVDGLWVWMEFLEGGALTDIVTHTRMNEEQIAA 120

QY 420 VCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTP 479
DB 121 VCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTP 180

QY 480 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPYFNEPPLKAMKMIKRDNLPPRLKNLH 539
DB 181 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPYFNEPPLKAMKMIKRDNLPPRLKNLH 240

QY 540 KVSFSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 241 KVSFSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292

RESULT 13
US-10-406-676-9
; Sequence 9, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyasamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT FILING DATE: 2003-04-02
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-9

Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 359
DB 1 SHEQFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 60

QY 360 RELLEFNEVIMRDYQHENVVEMVNSYLVDGLWVWMEFLEGGALTDIVTHTRMNEEQIAA 419
DB 61 RELLEFNEVIMRDYQHENVVEMVNSYLVDGLWVWMEFLEGGALTDIVTHTRMNEEQIAA 120

QY 420 VCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTP 479
DB 121 VCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTP 180

QY 480 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPYFNEPPLKAMKMIKRDNLPPRLKNLH 539
DB 181 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPYFNEPPLKAMKMIKRDNLPPRLKNLH 240

QY 540 KVSFSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 241 KVSFSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292

RESULT 14
US-10-406-676-10
; Sequence 10, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyasamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT FILING DATE: 2003-04-02
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-10

Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 359
DB 1 SHEQFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKKMDLRKQOR 60

QY 360 RELLEFNEVIMRDYQHENVVEMVNSYLVDGLWVWMEFLEGGALTDIVTHTRMNEEQIAA 419
DB 61 RELLEFNEVIMRDYQHENVVEMVNSYLVDGLWVWMEFLEGGALTDIVTHTRMNEEQIAA 120

QY 420 VCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTP 479
DB 121 VCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTP 180

QY 480 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPYFNEPPLKAMKMIKRDNLPPRLKNLH 539
DB 181 YWMAPELISRLPYGPEVDIWSLGIWVEMVDGEPYPYFNEPPLKAMKMIKRDNLPPRLKNLH 240

QY 540 KVSFSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 241 KVSFSLKGFLLRDLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 292

RESULT 15
US-10-406-676-11
; Sequence 11, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
```

```

; APPLICANT: Antonyamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-11

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Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEQFRAALQLVVDPGDPRSILDNFIKIGEGSTGIVCIATVRSSGKLVAVKXMDLRKQOR 359
Db 1 SHEQFRAALQLVVDPGDPRSILDNFIKIGEGSTGIVCIATVRSSGKLVAVKXMDLRKQOR 60

QY 360 RELLENEVIMEDYOHENNVENMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAA 419
Db 61 RELLENEVIMEDYOHENNVENMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAA 120

QY 420 VCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTGTP 479
Db 121 VCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTGTP 180

QY 480 YWMAPELISRLPYGPEVDIWSLGINVMEVMDGEPYFNEPPLKAMKIRDNLPRLKNLH 539
Db 181 YWMAPELISRLPYGPEVDIWSLGINVMEVMDGEPYFNEPPLKAMKIRDNLPRLKNLH 240

QY 540 KVSPLKGLFDRLVDRPAQRATAELLKHPFLAKAGPPASTIVPLMRQNRTR 591
Db 241 KVSPLKGLFDRLVDRPAQRATAELLKHPFLAKAGPPASTIVPLMRQNRTR 292

```

Search completed: September 29, 2004, 18:09:25  
Job time : 150.75 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 17:57:52 ; Search time 43.4559 Seconds  
(without alignments)  
1308.205 Million cell updates/sec

Title: US-10-693-367-2  
Perfect score: 3090  
Sequence: 1 MFGKKKKVEISAPSNFEHR.....LAKAGPPASIVLMKQNRTR 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1096.5	35.5	540	2	T19956
2	1090.5	35.3	542	2	T19952
3	917	29.7	544	2	A57597
4	907	29.4	544	2	I49376
5	895.5	29.0	525	2	S58682
6	892.5	28.9	545	2	G01773
7	892	28.9	544	2	S40482
8	846.5	27.4	1230	2	T18256
9	846.5	27.4	1230	2	T18259
10	837	27.1	939	2	S28394
11	823.5	26.7	658	2	T39500
12	814.5	26.4	658	2	S60170
13	811.5	26.3	622	2	T15467
14	760	24.6	842	2	S60402
15	722	23.4	378	2	T26684
16	697	22.6	589	2	T38086
17	651.5	21.1	655	2	S51894
18	505	16.3	836	2	B96716
19	498	16.1	471	2	T39232
20	494	16.0	1102	2	JC6316
21	478	15.5	653	2	T34356
22	476	15.4	819	2	A53714
23	470.5	15.2	829	2	T29372
24	464	15.0	426	2	S71886
25	463	15.0	1231	2	T18532
26	462	15.0	1233	2	T14157
27	460	14.9	1206	2	T34021
28	458.5	14.8	690	2	C96572
29	455.5	14.7	1080	2	S48944

30 455 14.7 1233 2 T30989 serine/threonine p  
31 450.5 14.6 312 2 T38525 serine/threonine p  
32 445 14.4 1001 2 T17365 serine/threonine p  
33 440.5 14.3 1075 2 T27623 hypothetical prote  
34 440.5 14.3 1080 2 T27622 hypothetical prote  
35 437.5 14.2 1062 2 S46367 protein kinase CDC  
36 428 13.9 1228 2 T18897 hypothetical prote  
37 424.5 13.7 659 1 A39723 protein kinase byr  
38 421 13.6 553 2 T01479 hypothetical prote  
39 419 13.6 883 2 A96662 hypothetical prote  
40 417.5 13.5 1174 2 T43051 protein kinase C (p  
41 413 13.4 561 2 T51417 protein kinase-lik  
42 409.5 13.3 652 2 T39722 serine/threonine p  
43 409 13.2 891 2 T40503 protein kinase kin  
44 405.5 13.1 1139 1 S61918 protein kinase C (p  
45 404.5 13.1 1135 1 A29813 132K ninaC protein

ALIGNMENTS

RESULT 1  
T19956  
Hypothetical protein C45B11.1b - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T19956  
R:McMurray, A.  
Submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19202  
A:Accession: T19956  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-540 <WIL>  
A:Cross-references: EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C45B11.1b  
A:Experimental source: clone C45B11  
C:Genetics:  
A:Gene: CESP:C45B11.1b  
A:Map position: 5  
A:Introns: 13/2; 62/3; 104/2; 231/3; 367/2; 468/3  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 35.5%; Score 1096.5; DB 2; Length 540;  
Best Local Similarity 41.7%; Pred. No. 1.4e-31;  
Matches 251; Conservative 67; Mismatches 151; Indels 133; Gaps 9;  
QY 4 KRKRVEISAPSNFEHRVHTGFDQHQKFTGLPRQWSLI--ESARRPKPLVDPACITS 61  
Db 29 RKVKSEISTPSNFEHRIHAGFDARS GTY TGLPKQWQALLGPPRSISRPKPMVDPSCITP 88  
QY 62 IQFGAPKTIVRGSKGAKGAKGALITLLDDEFNMSTRNSLRDPPPPPARARQNGMPEEP 121  
Db 89 VDVAELKTVIRGSSRYNSPLPFGMTNSPMSVARNSLRISATASP----- 135  
QY 122 ATTARGGCGRAGSRGRFAGHSEAGGSGDGRRRRAGPEKRPKSSREGSGGPOESSRDKRPLS 181  
Db 136 -----VVNVSSARHSFRPTLPVVSQR----- 156  
QY 182 GPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEHDVAPNGSPSAGGLAIPQ 241  
Db 157 -----GYPF-----NDPSVAPLPL-- 170  
QY 242 SSSSSSRPPTFRAGAPSGVLGPH-----ASEPQLAPPACTEAPAPVPGPG 288  
Db 171 ---RNQKPPM---STTFGVEKHQOQIITIVAPSRITTPLOPKS-----PST 213  
QY 289 PRSPQREP---QRVSHQFRAALQLVDPDGPSPSYLDNFIKIGEGSTGIVCIATVRSRGK 345  
Db 214 PQMRQPKCTEGVSDEEFNALKFVVDGTDPRSLLTDYKQIGEGSTGVVEAAAYKISTKQ 273  
QY 346 LVAVKGMDLRKQQRRELLFNEVIMRDYQHENVVMTNSYLVDGLVWVMEFLEGGALTD 405  
Db 274 IVAVKRMNLAKQQRRELLFNEVILRQYQHPNIVRRFSSHLVDDELKVVWMEFMEGGSLTD 333

406	Qy	IVTUTRMNEQIAA	VCVLAVLQALS	VHLAGQV	IHRDI	KSDSI	LLTHDGR	VKLSDFG	CAQV	465
334	Db	IVTATRMTEPQI	ATISRQVLGALD	FLHARKV	IHRDI	KSDSI	LLKRDGT	VKLTDFG	CGQL	393
466	Qy	SKEVPRRKS	LVCTPYWMAPE	LISRLPYG	PEVDI	WSLGM	VIEMWDG	PEPFYNE	PEPKAMK	525
394	Db	SEEVPRRKS	LVCTPYWTA	AEIAREPY	TDRAI	WSFGIM	LIEVMWGE	PEPFYNDQ	PQFQAMK	453
526	Qy	MIRONL	PPRLKNLHKV	SPSLKGF	LDRLAVRD	PAQRATA	EALLKHP	EFLAKAG	PPASTIVPLM	585
454	Db	PIRDEH	EARFESHAKV	SVLS	SELLSHCH	IVKDNK	WPAKDL	LURHP	FFAKAQHSS	513
586	Qy	RQ	587							
514	Db	LQ	515							

RESULT 2  
T19952  
hypothetical protein C45B11.1a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T19952  
R:McMurray, A.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19202  
A:Accession: T19952  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-542 <WIL>  
A:Cross-reference: EMBL:Z74029; PIDN:CAA98429.1; GSPDB:GN00023; CESP:C45B11.1a  
A:Experimental source: clone C45B11  
C:Genetics:  
A:Gene: CESP:C45B11.1a  
A:Map position: 5  
A:Introns: 13/2; 62/3; 104/2; 233/3; 369/2; 470/3

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Query Match      35.3%; Score 1090.5; DB 2; Length 542;
Best Local Similarity 42.0%; Pred. No. 2.3e-31;
Matches 253; Conservative 69; Mismatches 149; Indels 131; Gaps 11;

QY      4 KRKRKRVISAPSNFEHVRHVFQDOHQEQKFTCLPQWQSLI--ESASRRPKPLVDPACITS 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      29 RKVKSEISTPSNFEHRIHAGFDARSQTYTGLPKQWQALLGPPRSISRPKPMVDPSCITP 88
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      62 IQGAPKTIIVRGSKCAKDGAITLLLDDEFENMSVTRNSLRRDPPPPARARQENGMPEEP 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      89 VDVAELKTVIRGP-----SSSFYNSPLP-----FGMTNSP 119

QY      122 ATTARGGFKVAGSGRGRFAGHSEAGGGSDRRRRAGPEKRPKRSRRGGSGPOESSRDKRPLS 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      120 MPVS-----ARNSLSLRI SATASPVVNVSSARHSFRPTLPPVSQR----- 158

QY      182 GPDVGTGPQAGLASGAKLAAGRPNITYPRADTDHPSRGAQGERHDVAPNGPSAGGLAIPO 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      159 -----GYPP-----NDPSVAPLEPL----- 172

QY      242 SSSSSSRPPTARGAPSPGVLGPH-----ASBPQLAPPACTPAAPAVPQPPG 288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      173 ---RNQKPFM---STTFGEVKEPHYQQIITIVAPSRSTTTTLPQPKS-----PST 215

QY      289 PRSPQREP---QRVSHQEFRAALQLVDPGDPRSFLDNFIKIGBSGTIVCIATVRSQK 345
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      216 PQAMQQPKCTEGVSDSEFNALKFVVDGTDPRDSDLTDYKQIGEGSTGVVVEAYAKISTKQ 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      346 LVAVKMDLAKQQRRELLFNEMTMRDYGHEVNVEMYSVLVGDMLVVMVEFLGGALTD 405
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      276 IVAVKRMNLKQQRRELLFNEMSLRQYQHPNIVRFSSHVLVDDELVVMVEFWEGSLTD 335
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      406 IVVTHTRMNERQIIAAVCLAVIQAQSLVLAHQGVIVHRDITKSDSILITHDGRVKLSDFGFCQV 465
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db	336	IVTATRMTEPQIATISRQVLGALDFLHARKVTHRIDIKSDSIILLKRDGTVKLTDGFQCGQL	3395
Qy	466	SKEVPRRRKSLVGTPTWMAPELISRLPYGPEVDIWSLIGIMVIEWMDGEPYFVNEPPPLKAMK	5255
Db	396	SEEVPRRRSLVGTPTWTAEEVIAREPYDTRADISFGIMLIEWEGEPFFFNDDPQOAMK	4555
Qy	526	MIRDNLPPRLKNLHKSPLSKGFLDELIVDRDPAQRATAAELLKHPLAKAGPPASTIVPLM	5855
Db	456	RIRDEHEARFSHAKVSVELSELLSHCHIVKOVNKEWPAKDLLRHFFFAKAQHSSSIAPLL	5155
Qy	586	RQ 587	
Db	516	LO 517	

### RESULT 3

A57597  
 Beta-p21-activated protein kinase - rat  
 N:Alternate names: beta-PAK  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 24-Sep-1999  
 C:Accession: A57597  
 R:Manser, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L.  
 J. Biol. Chem. 270, 25070-25078, 1995  
 A:Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK)  
 A:Reference number: A57597; MUID:96027610; PMID:7559638  
 A:Accession: A57597  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-544 <MAN>  
 A:Cross-references: GB:U33314; NID:G1039424; PIDN:RACS2268.1; PID:G1039425  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol  
 C:Keywords: ATP  
 F:2666-519/Domain: protein kinase homology <KIN>  
 F:274-282/Region: protein kinase ATP-binding motif

[illegible]



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Db 424 GTPYMADEVVTRKAYGPKVDLWSUGIMAEWVEGEPYLNENPLRALYLATNGTPELQ 483
QY 537 NLHKVPSLKGFLDRLVDRPAQATAAEALLKHPFLAKAGPPASIVPLM 585
Db 484 NPERLSAVFRDFLNRCLMDVDVRRGSAKELLQHPFLKAKPLSSUTPLI 532

RESULT 4
149376
p21 activated kinase-3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I49376
R:Bagrodia, S.; Taylor, S.J.; Creasy, C.L.; Chernoff, J.; Cerione, R.A.
J. Biol. Chem. 270, 22731-22737, 1995
A:Title: Identification of a mouse p21cdc42/Rac activated kinase.
A:Reference number: I49376; MUID:96032693; PMID:7559198
A:Accession: I49376
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-544 <RES>
A:Cross-references: EMBL:U39738; NID:g1079713; PIDN:AAC52354.1; PID:g1079714
C:Genetics:
A:Gene: mPAK-3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP
F:266-519/Domain: protein kinase homology <KIN>
F:274-282/Region: protein kinase ATP-binding motif

Query Match 29.4%; Score 907; DB 2; Length 544;
Best Local Similarity 34.6%; Pred. No. 4.7e-25;
Matches 204; Conservative 90; Mismatches 169; Indels 126; Gaps 7;

QY 4 KRKRVEISAPSNFHRVHTGFDQHQKFTGLPRQMSLIE-----ESARRPKPLVDP 56
Db 63 KEKERFEISLPDFEHTIHVGFDAVGTGFTGPEQWARLLQTSNITKLEQKNPQAVLD- 121
QY 57 ACITSIQGAPKTIIVRGSKAGKDGALTLLDDEFNNMSTRSLRDSPPPPARARQENG 116
Db 122 -----VLKFDYSKETVNNQKMSFT----- 141
QY 117 MPEEPATTARGGPKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPQESSRD 176
Db 142 -----SGDKSAHGVIYAAHQ-----SWTKTGSPEPLAPPVSEHEDEEEBDD 184
QY 177 KRPLSGPDVGTPOPGAGLSAGKLAAGRPFTYPRADTDHPSRGAQGEHDVAPNGPSAGG 236
Db 185 NEP---PPVIAPRPHTKS-----IYTRSVVESIASPAAPNKEDIPPSAENANS 230
QY 237 LAIPQSSSSSRPPTRRARGAPSPGVLGPHASEPQLAPPACTPAAPVPGPPGPRSPQREP 296
Db 231 TTLRYNTDR-----QRKK 243
QY 297 QRVSHSEQFAALQLVDPDPRSYLDNFIKIGSGSTGIVCIATVRSGKLVAVKQMDLRK 356
Db 244 SKMTDBEILEKLSIVSGVDPKKYTKLEKIGQASGTVTALDIATGQEVAKLQKMLQQ 303
QY 357 QORRELLFNEWIMRDYQHENVVMYNSYLVGDELWVMEFLEGALTDIVTHTRMNEEQ 416
Db 304 QPKELLIINELVWRENKFNIVNYLDSYLVGDELWVMEYLAGSLTDVVVTETCMDVGQ 363
QY 417 IAAVCLAVLQALSVLHQAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVKEVPRRKSIV 476
Db 364 IAAVCRECLQALDPLHNSQVTHIRDIKSDNILLGMDGSKVLTDGFCQAQITPEOSKRSTMV 423
QY 477 GTPYMAPELISRLPYGPEVDIWSLGMVEMVDGEPPEYNEPPLKAMKMRDNLPLRLX 536
Db 424 GTPYMAPEVTRKAYGPKVDLWSUGIMAEWVEGEPYLNENPLRALYLATNGTPELQ 483
QY 537 NLHKVPSLKGFLDRLVDRPAQATAAEALLKHPFLAKAGPPASIVPLM 585
Db 484 NPERLSAVFRDFLNRCLMDVDVRRGSAKELLQHPFLKAKPLSSUTPLI 532
```

```
RESULT 5
S58682
protein kinase, p21-activated (EC 2.7.1.1.-) - human
N:Alternate names: protein kinase PAK65; S6/H4 kinase
C:Species: Homo sapiens (man)
C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 24-Sep-1999
C:Accession: S58682; S55258; S55304; S58690; A57441
R:Sells, M.; Knause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.
submitted to the EMBL Data Library, April 1995
A:Description: Human p21-activated protein kinases regulate actin organization in mamma
A:Reference number: S58682
A:Accession: S58682
A:Molecule type: DNA
A:Residues: 1-525 <SEL>
A:Cross-references: EMBL:U24153; NID:g780807; PIDN:AAA5442.1; PID:g780808
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.
EMBO J. 14, 1970-1978, 1995
A:Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation is
A:Reference number: S55258; MUID:95262637; PMID:7744004
A:Accession: S55258
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'MEETQOKSNLEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525 <
A:Accession: S55304
A:Molecule type: protein
A:Residues: 402-418 <MAW>
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.
EMBO J. 14, 4385, 1995
A:Reference number: S58690; MUID:96016211; PMID:7556080
A:Contents: erratum
A:Accession: S58690
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-30 <MAP>
R:Benner, G.E.; Dennis, P.B.; Masaracchia, R.A.
J. Biol. Chem. 270, 21121-21128, 1995
A:Title: Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular anc
A:Reference number: A57441; MUID:95403344; PMID:7673144
A:Accession: A57441
A:Molecule type: protein
A:Residues: 197-216; 402, 'S', 404-409 <BEN>
A:Experimental source: placenta
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin
F:247-501/Domain: protein kinase homology <KIN>
F:255-263/Region: protein kinase ATP-binding motif
F:197,402/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 29.0%; Score 895.5; DB 2; Length 525;
Best Local Similarity 34.9%; Pred. No. 1.1e-24;
Matches 211; Conservative 94; Mismatches 136; Indels 163; Gaps 14;

QY 4 KRKRVEISAPSNFHRVHTGFDQHQKFTGLPRQMSLIE-----ESARRPKPLVDP 56
Db 67 KEKERFEISLPDFEHTIHVGFDAVGTGFTGPEQWARLLQTSNITKLEQKNPQAVLD- 125
QY 57 ACITSIQGAPKTIIVRGSKAGKDGALTLLDDEFNNMSTRSLRDSPPPPARARQOE 114
Db 126 -----VLKFDY-----SNTVKQKYUSFTPP-----EK 147
QY 115 NGMPE-EPATTARGGPKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPQES 173
Db 148 DGLPSGTPLNAXG-----TEA-----PAVVEEEDDEET 178
QY 174 SRDKRPLSGPDVGTPOPGAGLSAGKLAAGRPFTYPRADTDHPSRGAQGEHDVAPNGPS 233
Db 179 A-----PPVIAPRPHTKS-----IYTRSVVID-PVPAPVGDH----- 210
QY 234 AGGLATPQSSSSSRPPTRRARGAPSPGVLGPHASEPQLAPPACTPAAPVPGPPGPRSPQ 293
Db 211 -----VDGAAKSLDKQ 221
```

Qy	294	REPORSVHQFRAALQLVVDQDPRSILDNFTIKIGESTGIYCIATVRSSGKLVAVKQMD	353
Db	222	KKKPKMTDEEIMKELRTIVSGDPKKKYTRYEKIQGASGTVPFATDVALGOEVAIKQIN	281
Qy	354	LRKQORRELLFNEVVMIRDYQHENVVMYNSYLVDGLWVWMEFLEGGALTDIVVTHR-M	412
Db	282	LQKQPKKELIINEILVMKELKNPNLVNFDLSVLVDGELFVWMEYLAGGSLLTDVVTEACM	341
Qy	413	NEEQIAAVCLAVLOALSVLHQGVTHRDIKDSIILTHDGRVKLSDFGCAQSVKEVPRR	472
Db	342	DEAQIAAVCRECLOALEFLHANQVTHRDIKSDNVLLGMEGSVKLTDFGCAQITPEQSKR	401
Qy	473	KSLVGTPTVWMAPELISRLPYGPEVDIWSLIGIMVIEWDGEPYPFNEPPLKAMKMIRNLP	532
Db	402	STMVGTPTVWMAPEVVTTRKAYGPKVDIWSLIGIMAIEMWGEPEPPLNENPLRALLYLATNGT	461
Qy	533	PLRNLNLHKVPSLKGFLDRLLVRDPAQATATAELLKHPFLAKAGPPASTVPL-----M	585
Db	462	PELQNPKEKLSPTFRDFNLNRCLEMDVEKGSAXELLOHFLKLAKPLUSLTPLIMAAKEAM	521
Qy	586	QQRN	589
Db	522	KSNR	525

RESULT 6  
G01773  
p21-activated protein kinase - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 24-Sep-1999  
C/Accession: G01773  
R;Chernoff, J.  
submitted to the EMBL Data Library, April 1995  
A;Reference number: G08374  
A;Accession: G01773  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-545 <CHE>  
A;Cross-references: EMBL:U24152; NID:g780805; PID:AAA65441.1; PID:g780806  
C;Genetic:  
A;Gene: Pak1  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo  
F;268-521/Domain: protein kinase homology <KIN>

Query Match	28.9%	Score	892.5	DB 2	Length	545			
Best Local Similarity	36.9%	Pred. No.	1.5e-24						
Matches	216	Conservative	82	Mismatches	166	Indels	121	Gaps	11
QY	4	KRKKRVEISAPSFHEHVHTGFDQHEQKFTGLPRQWSLIEESARRPKPLVDPACITSIQ	63						
Db	68	KEKERTFISPSDFEHTIHVGFDAVTEFTGPMCEQWARLLQTSN	111						
QY	64	PGAPKTVIRGSGKAGKOGALTLILLDEFENMSTRNSLRDRSPPPPARAQENGMPPEEPAT	123						
Db	112	-----ITKSEQKNPQAVLDLVLEFYNSKKT-SNSQKYS-----	144						
QY	224	TARGGFKAGSRGRFPAGHSAGGGSGDRRRAGPEKPKSRREGSGGPOESSDRKRPLSGP	183						
Db	145	-----FTDKSAEDYNSSNALNV-----KAVSETPAVPVSEDED-----	181						
QY	184	DVGTPOPGAGLAKLAAGRPENT-----YPRADTDHPSRGAGEPHDVAPNGPFSAGGLAIP	240						
Db	182	DDATPPP-----VIAPPEHKSVYTSVI-----BPLVPTPT-----	214						
QY	241	QSSSSRRPPTRAGAPSPGVLGPHASEPQLAPPACTPAAPVAPGPGPSPRSPQREPQVRS	300						
Db	215	RDVATSPISPTENNTTP-----PDALTENT-----EKQKKKPKMS	249						
QY	301	HEQFRAALQLVDPGDRSPRLDNFIKIGESTGIVCIATVRSSGLKVAVKQMDLRKQRR	360						
Db	250	DEBIEKLRSIVSGDPKKKYTFEKGQASGVTYAMDVATQOEVAIKQMLQQQPPK	309						

QY	361	ELLFNEVVIMRDYQHENVEMVNSVLVDGELVWVMFELEGGALTDIVTHTRMNEEQIAAV	4200
Dd	310	ELIINEILVMRENKPNINVTLDLSVLVDGELVWVMVEYLAGSLTDVTWTCDMEGQIAAV	3698
QY	421	CLAVLQALSVLHAOGVTHRDIKSDISILLTHDGRVKLSDFGCAOVSSKEVPKRKSLVGTPY	4800
Dd	370	CRECLQALEFTJHSNQVTHRIDIKSDNILGMDSGVKLDTGFCAQTTPSQSKSTVWGTPY	4298
QY	481	WMAPELISRPLPGPEVIDTWSIGIMVIENVDGEPPPYFNFPPLKAMKMIRDLNLPRLKNLHK	5400
Dd	430	WMAPEVTVTKAYGPKVDIWSLGIMAIEMIEGEPYVLNENPLEALYLIATNGTPELQNPEK	4898
QY	541	VSPSLKGFLDRLLVRDPQAORTAAEELLKHFFLAAGPASPASIVPLM	585
Dd	490	LSAIFRDFLNRLCNDMDVEKRGSAKELLQHQLFKIAKPLSSLTPLI	534

RESULT 7  
S40482 serine/threonine-specific protein kinase (EC 2.7.1.-) - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C/Accession: S40482  
R/Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.  
Nature 367, 40-46, 1994  
A/Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.  
A/Reference number: S40482; PMID:94150588; PMID:8107774

## RESULT 7

S40482  
serine/threonine-specific protein kinase (EC 2.7.1.-) - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C;Accession: S40482  
R;Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.  
Nature 367, 40-46, 1994  
A;Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.  
A;Reference number: S40482; MUID:94150588; PMID:8107774  
A;Accession: S40482  
A;Molecule type: mRNA  
A;Residues: 1-544 <MAN>  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase  
C;Keywords: Arp; phosphotransferase; serine/threonine-specific protein kinase  
F;267-520/Domain: protein kinase homology <KIN>  
F;275-283/Region: protein kinase ATP-binding motif

Query Match	28.9%;	Score 892;	DB 2;	Length 544;
Best Local Similarity	36.9%;	Pred. NO. 1.5e-24;		
Matches 216;	Conservative	82;	Mismatches 165;	Indels 122; Gaps 11

QY	4	KRKRVEISAPSNFHRVHTGFDQHOEQKFTGLPRQWOSLIEESARRPKPLVDPACITSIQ	63
Db	68	KEKERHIEISLPSDFEHTIHVGFDCTGFTGMPQWARLLQTSN	111
QY	64	PGAPKTVIRGSKGAKOGCALTLLLDEPENMSTVRSLSLRROSPPPPAPARQENGMPBPAT	123
Db	112	-----ITKSEOKKNPQAVLDVLEFYSKKT-SNSQKYS-----	144
QY	124	TARGPGPKAGSRGRFAGHSAGGSGDRRRAGPEKPKSRREGSGGPOESSRDKRPLSGP	183
Db	145	-----FTDKSAEDYNSNTLNV-----KTVSETPAVPVSEDE-----	180
QY	184	DVGTPOBAGLASAKLAAAGPFNT--YPRADTHPSRGAQGEHVDVAPNGPSAGGLAIP	240
Db	181	DDATPPP-----VIAPREHTKSYVTRSVI-----EPLVTPT-----	213
QY	241	QSSSSSRPPTARGAPSPGVLFPHASEPQLAPPACTPAAPAVGPGPSRSPQRPQVS	300
Db	214	RDVATSPISPTENNTTP-----PDALTFRNT-----EKQKKPKMS	248
QY	301	HEQFRAALQVDPGDPSPRSLDNFIKIGEGSTGIVCIATVRSGLKVAVKKMDLKRQORR	360
Db	249	DEEILEKLRNVISVGDPKKKYTRFEKIGQCSGTVYTMADVATQGEVAIKQMNLOQOPKK	308
QY	361	ELLFNEWIVMRDQCHENVEMNSYLVGDELWVMEFLEGALTDIVHTRMNEBQIAAV	420
Db	309	ELINEILVMRENKNINVNYLDSYLVGDELWVMEYLAGSLTDVVTETCMDESGQIAAV	368
QY	421	CLAVLQALSVLHAQGVYIHRDIKSDSILLTHDGRVKLSDFGFCQVSKSEVPRRKSLVGTPEY	480
Db	369	CRECQALEFLHSNQVYIHRDIKSDNILLGMDGSKVLTDFFCAQITTEQSKRSTWVGTPY	428
QY	481	WMAPELISRLPYGPEVDIVNSLGHIMVTEMVDGPPYFNPEPLKAMKMTIRDNLPPRLKNLHK	540





142 RKSIVTSSPPDPKHVTHVGFNYDTGFTGMETEQALLKVSIGITKSEQVQHPOAVLDAMA 201  
59 ITSIQCAPKTIIVRGSKAKDGALTLLDEFENMSVTRSNLSRRDSSPPPPARARQNGMP 118  
202 FYS-----QSKKYLEGA-----KPPPRESTEK----- 225  
119 EEPATTARGPGKAGSRGRFAGHSEAGGSGDRRAGPEKRPKSSREGSGGQESSRDKR 178  
226 -----PLLSVSALSSSSHLQPTSATSSSSRLYP-----SR 255  
179 PLSGPDVGTPOPAGLAGAKLAAGRPFNTYPRADTDHPSRGAQGEPHD--VAPNGPSAGG 236  
256 P-----APTTPASSSSPLSSQTVKTTTNSASRQPSPLVSSKSTDNIIRSHSPV--- 305  
237 LAIPQSSSSSRPPTRARGAPSPGVLGPHASEP--OLAPPACTPAAPAVP-----GPPGPR 290  
306 LLTPQTLLTSETKHIR-----PNNSTPYQRRRAETSKPKAVATPKQVEAPSAPR 354  
291 SPOREPORVSEQ-FRAALQIVDPGDRPSYLDNFIKIGEGSTGIVCIATVRSSGKLAV 349  
355 LQKRAPQQNSDASVAKLOKICNPKNFTLLYRNFVKIGQASGDVYSARQVGTNLSVAI 414  
350 KMDLRKQQRRELLFNEVIMRDYOHENVMYNSLYVGDELWVMVEFLEGGALTIDIVTH 409  
415 KKNINOQPKKEFVINEILVWMSHHKKNVNFIDFFYKSELWVMWYWRGSSLTEVTN 474  
410 TRNNEQIAAVCLAVLQALSVLHAQGVIIHRDIKDSILLTHDGRVKLSDFGFCQAQSVKEV 469  
475 NTLSEGGIAAICKETLELYSLDHENGI VHRDIKDSNILLSQGDIKLITDFGFCQAQIDSNM 534  
470 PRKSLVGTTPWMAPELLISRLPYGPEVDIWSLIGIMVIEWVDEGPEPPYFNPPLKAMKMI 529  
535 TKPTTVMGTTPWMAPEVVRKEYGFKVDVWSLIGIMAEIEMVEGPEPPYLNENPULALYLIAT 594  
530 NLPLRLKNLHKVPSLKGFLDRLVDPDAQATATAELLKHPFLAKAGPPASIVPLMR 586  
595 IGTPIKSRPELLSSVFHDFLSKSLTVNPKQRPSSGELLKHPFLKQAVPVSSLLIPLIX 651

RESULT 13  
T15467  
hypothetical protein C09B8.7 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 19-May-2000  
C/Accession: T15467  
R/Stellives, L.  
submitted to the EMBL Data Library, June 1995  
A/Description: The sequence of C. elegans cosmid C09B8.  
A/Reference number: S61138  
A/Accession: T15467  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-622 <STE>  
A/Cross-references: EMBL:U29612; NID:g868273; PID:g868279; PIDN:AAA68805.1; CESP:C09B8.7  
A/Introns: 107/1; 142/3; 192/1; 260/3; 291/3; 481/1; 505/3; 546/3; 570/3  
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 26.3%; Score 811.5; DB 2; Length 622;  
Best Local Similarity 33.7%; Pred. No. 1e-21;  
Matches 207; Conservative 87; Mismatches 175; Indels 145; Gaps 15;

Qy 4 KRKKEVE-----ISAPSNFEHRVHTGFDQHEQFTGLPROMQSLI-----EESARRPKP 52  
109 KDKKEASEKPVISRPSNFETHIVGYDPKGTGTMPEAWARLLTDSQISKQEQQQPQA 168  
53 LVDPACTISIQGAPKTIIVRGSKAKDGALTLLDEFENMSVTRSNLSRRDSSPPPPARAR 112  
169 VLD-----ALKYYTQGESGSGKWLQYDNDAPSRTPSYCLK----- 204  
113 QENGMPPEEPATTARGPGKAGSRGRFAGHSEAGGSGDRRAGPEKRPKSSREGSGGQEQ 172

Db 205 -----PQP 207  
QY 173 SRSRKLSPDVGTPQAGLASGAKLAAGRPTTYPRADTDHPSRGAQGEPHDVA PNGP 232  
Db 208 YTSLSLYHGKIQDPRKNWPTTSSAG--YNS-----KQGV-----P 246  
QY 233 SAGGLAIPSSSSSSRPPTTRARGAPSPGVLGPHASEP-OLAPPACTPAAPA-----282  
Db 247 TTFSV-----NENRSSMPPSY---APP---VPHGETPADIVPPA-TPDRPARTLSIYTKP 295  
QY 283 -----VP-----GPPGPRS-PQREPORVSHQEPRAALQVLVDPGDRSRLDNFIKIGEGS 331  
Db 296 KEEEEKIPDLSKQGFQVARGQAKKMTDAEVLTKLRTIVSIGNDRKYRKVDKIGSGA 355  
QY 332 TGIIVCIATVRSRGLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMYSYLVDGL 391  
Db 356 SGSVYTAISISTAEVAIKQMLKQDPKKEILINELVWRENKHANIVNLSYLVCDL 415  
QY 392 WVMEFLEGALTDIVTHTRMBEQIAAACLAVLQALSVLHAGQVHHRDIKSDSILLTHD 451  
Db 416 WVMEYLAGSLTDVVTECOMEDGIIAAVCREVLQALEFLHSRHHVHRDIKSDNILLGMD 475  
QY 452 GRVKLSDFGFCQVSKVEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLIGIMVMDG 511  
Db 476 GSVKLTDFGCAQLSPEQRKRTTVMGTPTWMAPEVVTYKQYGPKVDVWSLIGIMAEWEG 535  
QY 512 EPPYFNEPPLKAMKMRDLNLPRLKNLHKVSPSLKGLFDRLLVDRDPAQRATAELLKHPF 571  
Db 536 EPPYLNENDLRIALYLIATNGKDFDGRDSMTLLFKDFVDSALEVQVENRWSAQLLTHPF 595  
QY 572 LAKAGPPASIVPLM 585  
Db 596 LRCAPLASLYYLI 609  
RESULT 14  
S60402  
protein kinase CLA4 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)  
N/Alternate names: protein N0450; protein YNL0450; protein YNL298W  
C/Species: Saccharomyces cerevisiae  
C/Date: 27-Apr-1996 #sequence revision 17-May-1996 #text\_change 24-Sep-1999  
C/Accession: S60402; S63274; S53103  
R/Maurer, K.C.T.; Urbanus, J.H.M.; Planta, R.J.  
Yeast 11, 1303-1310, 1995  
A/Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a  
C, and a novel putative serine/threonine protein kinase gene.  
A/Reference number: S60394; PMID:96132033; PMID:8553702  
A/Accession: S60402  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-842 <MAU>  
A/Cross-references: EMBL:U23084; NID:g1050853; PIDN:ACA49100.1; PID:g1050862  
R/Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.  
Submitted to the Protein Sequence Database, April 1996  
A/Reference number: S63266  
A/Accession: S63274  
A/Molecule type: DNA  
A/Residues: 1-842 <MAU>  
A/Cross-references: EMBL:Z71574; NID:g1302389; PIDN:CAA96216.1; PID:e239731; PID:g130239  
A/Experimental source: strain S288C  
R/Cvrckova, F.; Naemlyth, K.  
Submitted to the EMBL Data Library, November 1994  
A/Description: STE20-like protein kinases are required for cytokinesis.  
A/Reference number: S53103  
A/Accession: S53103  
A/Molecule type: DNA  
A/Residues: 1-389, I', 391-842 <CVR>  
A/Cross-references: EMBL:X82499; NID:g732943; PIDN:CAAS7879.1; PID:g732944  
A/Experimental source: strain K1107  
C/Genetics:  
A/Gene: SGD: CLA4; ERC10  
A/Cross-references: SGD:S0005242; MIPS:YNL298W

A/Map position: 14L  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; pleckstrin repeat hom  
C/Keywords: ATP; phosphotransferase  
F;544-825/Domain: protein kinase homology <KIN>  
Query Match 24.6%; Score 760; DB 2; Length 842;  
Best Local Similarity 31.2%; Pred. No. 7.6e-20;  
Matches 212; Conservative 99; Mismatches 239; Indels 130; Gaps 23;  
QY 11 ISAPSNFHRVHTGDQHEQKFTGLPRQWSLIESARRPKPLVD--PACISIQ-----63  
Db 184 VSSPTNFTKHVGDPEPTGSEFVGMPTNWEKLLKHSRITCEDWNNSAAVIOVLQFYQY 243  
QY 64 --PGAPKTVIRGSKGAKGALILLDEPENMVSVTRNSL-----RDSRP 106  
Db 244 NGAGNPTNTLDKPSGETSSSKSLPNSYNDKNLNNSVNSKSSGVSVMWSQRKTSQP 303  
QY 107 PPARARQENG-----MPEEPATTAR---GGFGKAGSRGRFAGHSEAGGSDRRR 153  
Db 304 PNTKGFVSLGSLPPIINTKLPTSQSNIPRHLQNVNQYPKMR-NGHSPITNG---QFP 358  
QY 154 AGPEKPKSSRSGSGGPOESSRDKP-----LSGPDVGTTPQAGLAGAKLAAGRP 206  
Db 359 RGMHPNNSQRSLOQQQQQQQQKQHQYYPYHQQP---SPSPSPSPS-----PLN 407  
QY 207 TYPRADTDHPSRGAQGEPHDVA PNGP---SAGGLAIPSSSSSSSRPPTRA----RGAP 257  
Db 408 PY-----RPHN-MINPYSKOPQPLSSQSTQNOAIPRYAQNSS--PTAAHFPOPTAP 458  
QY 258 SPGVGLPHASEPQ-----LAP-----PACTPAAPAVP---GPGGPRSPQRE 295  
Db 459 KPPI SAPRAPYPSNQNATSNTHVQVPAPKNDQSTQTMRQAPKRPDADVAQGGVAKPKK 518  
QY 296 POR--VSHEQFRAALQVLVDPGDRSRLDNFIKIGEGSTGIVCIA-----TWRSS-----343  
Db 519 PARPTMSTAETMSKLVKVTVNADPSQCFKVIKAGQAGSGSYLAERTHIPTESNMIELI 578  
QY 344 -----GKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMYSYL-VGDELWV 393  
Db 579 NNDIDEPHVGDVAKLVQWVLSKQPKKELLVNEILVWKSRRHKNIVNFEAYLRTDLDLWV 638  
QY 394 VMEFLEGALTDIV-----THTRMBEQIAAACLAVLQALSVLHAGQVHHRDIKSDS 445  
Db 639 VMEFMEGGSLTDIENSPTNDNSHPLTEPQIAYIVRETCCGLKFLHDKHIIHRDIKSDN 698  
QY 446 ILLTHDGVKLSDFGFCQVSKVEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLIGIMV 505  
Db 699 VLLDTRARVKITDFGFCARLTDKRSKRATMVGTPYWMAPEVVKQREYDEKIDVWSLIGIMT 758  
QY 506 IMVDGEPYPFNEPPLKAMKMRDLNLPRLKNLHKVSPSLKGLFDRLLVDRDPAQRATAAE 565  
Db 759 IEMLEGEPPYLNEDPLKALYLIATNGTFLKHKHPESLSLEIKRFLSVCLVDVRYRASTEE 818  
QY 566 LKHKPFLAKAGPPASIVPLM 585  
Db 819 LLHHGFFNMACDPKDLTSLI 838  
RESULT 15  
T26684  
hypothetical protein Y38F1A.10 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C/Accession: T26684  
R/Wallis, J.  
submitted to the EMBL Data Library, October 1998  
A/Reference number: Z20253  
A/Accession: T26684  
A/Status: preliminary; translated from GB/EMBL/DBDJ  
A/Molecule type: DNA  
A/Residues: 1-378 <WIL>  
A/Cross-references: EMBL:AL032639; PIDN:CAA21637.1; GSPDB:GN000020; CESP:Y38F1A.10  
A/Experimental source: clone Y38F1A



C:Genetics:  
A:Gene: CESP:X38F1A.10  
A:Map position: 2  
A:Introns: 43/3; 221/2; 259/2; 309/3; 347/2  
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 23.4%; Score 722; DB 2; Length 378;  
Best Local Similarity 45.3%; Pred. No. 8.2e-19;  
Matches 143; Conservative 61; Mismatches 110; Indels 2; Gaps 2;

QY 277 TPAAPAVPGPPGPGSPQRPQSVHSQFRAALQLVVDPDPRSVDNFIKIGEGSTGIVC 336  
Db 64 TTVEPPPEEPVVRASHREKLSDEVLNQLREIVNPSNPLGKYEMKKQIGVGASGTVF 123

QY 337 IATVRSSGKLNAVKKMDLRKQRRRELLFNEVVIMRDYOHENNVEMNSYLV-GDELWVVM 395  
Db 124 VANVAGSTDVAVKRMFAKTPQKEMLLTEIKVMKQYRHPNLVNYIESYLVADADDLWVVM 183

QY 396 EFLEGGALTDIVTHTMNEEQIAAVCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVK 455  
Db 184 DYLEGNTDVVVVKTELDGQIAAVLQECALKHFLHRHSIVHRDIKSDNVLGMNGEVK 243

QY 456 LSDFGFCAQVSKEVPRKSLVGTPTVWMAPELISRLPYGPEVDIWSLGINVIMVDGEPY 515  
Db 244 LTDMGFCAQI-QPGSKRDVVGTPYWSPEILNKQYNYKVDIWSLGINALEMIDGEPY 302

QY 516 FNEPPLKAMKMTDNLPPRLKNLHKVPSLKGFLDRLLVRDPAQRATAAEILKHPFLAKA 575  
Db 303 LRETPLKATYLIAQNGKPEIKQDRLSSEFNFLDKCLVVDPDQADTTTELLAHPFLKKA 362

QY 576 GPPASIVPLMRQNRTR 591  
Db 363 KPLSSLIPYIRAVREK 378

Search completed: September 29, 2004, 18:05:37  
Job time : 47.4559 secs

Blank

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:41:57 ; Search time 133,844 Seconds  
(without alignments)  
1393.197 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGRKKRVEISAFNSFHR.....LAKAGPPASIVPLMRQNRTR 591

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2860	92.6	593	11 Q8BTW9	Q8btw9 mus musculus
2	2853	92.3	593	11 Q80Z97	Q80z97 mus musculus
3	2558	82.8	501	4 Q8N4E1	Q8n4e1 homo sapien
4	2202.5	71.3	467	4 Q9ULS8	Q9uls8 homo sapien
5	2202.5	71.3	483	4 Q8NDE3	Q8nde3 homo sapien
6	2124.5	68.8	650	13 Q90W62	Q90w62 xenopus lae
7	1967	63.7	407	11 Q8K0U2	Q8k0u2 mus musculus
8	1748	56.6	719	11 Q8C015	Q8c015 mus musculus
9	1740	56.3	719	11 Q8BVB0	Q8bvb0 mus musculus
10	1731	56.0	719	4 Q8TB93	Q8tb93 homo sapien
11	1501.5	48.6	639	5 Q9VXE5	Q9vxe5 drosophila
12	1497.5	48.5	639	5 Q960J8	Q960j8 drosophila
13	1497.5	48.5	639	5 Q96372	Q96372 drosophila
14	1241	40.2	240	4 Q8NCH5	Q8nch5 homo sapien
15	1160	37.5	229	11 Q9CS71	Q9cs71 mus musculus
16	1096.5	35.5	540	5 Q9U3M1	Q9u3m1 caenorhabdi

#### ALIGNMENTS

#### RESULT 1

Q8BTW9 PRELIMINARY; PRT; 593 AA.

AC Q8BTW9; 01-MAR-2003 (Tremblrel. 23, Created)

DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Serine/threonine-protein kinase PAK 4 (Similar to

DE p21(CDKN1A)-activated kinase 4).

GN PAK4 OR 5730488L07RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RC MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;

RC Strausberg R.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK088512; BAC40396.1; -

DR EMBL; BC048238; AAH48238.1; -

DR MGD; MGI:1917834; Pak4.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000035; PAKbox/Rho-binding.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_kinase.

DR InterPro; IPR001245; Tyr\_kinase.

Q18637 caenorhabdi  
Q9vi13 drosophila  
Q24190 drosophila  
Q24213 drosophila  
Q8kl16 mus musculus  
Q80320 brachydanio  
Q8kl15 mus musculus  
Q8axb4 xenopus lae  
Q8cin4 mus musculus  
Q72328 homo sapien  
Q7yql4 pan troglod  
Q7yql3 pongo pygma  
Q8aw67 brachydanio  
Q9p0j8 homo sapien  
Q9gyu0 rattus norv  
Q9ic2 xenopus lae  
Q728e9 magnaporthe  
Q9yeb5 homo sapien  
Q96uh9 magnaporthe  
Q75561 homo sapien  
Q9pw62 xenopus lae  
Q13431 candida alb  
Q9hew4 cryptococcu  
Q57318 xenopus lae  
Q8nk62 ustilago ma  
Q8x1f0 cryptococcu  
Q9p496 yarrowia li  
Q9hew5 cryptococcu  
Q9uv59 cryptococcu

DR Pfam; PF00786; PBD; 1.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00285; PBD; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR SMART; SM00219; TyRK; 1.  
DR PROSITE; PS0108; CRIB; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW Kinase.  
SQ SEQUENCE 593 AA; 64622 MW; 4AFA91DD73D4C6D5 CRC64;  
  
Query Match 92.6%; Score 2860; DB 11; Length 593;  
Best Local Similarity 92.6%; Pred. No. 4.6e-191;  
Matches 550; Conservative 10; Mismatches 30; Indels 4; Gaps 2;  
  
QY 1 MFGKKKVEISAPNFEHRVHTGFDQHEQKFTGLPRQWSLIESARRPKPLVDPACIT 60  
Db 1 MFGKKKVEISAPNFEHRVHTGFDQHEQKFTGLPRQWSLIESARRPKPLVDPACIT 60  
  
QY 61 SIQGPACTIIVRGSKGAKDGLTLLDDEFNMSVTRSNLSRRDPPPPARARQENMPPEE 120  
Db 61 SIQGPACTIIVRGSKGAKDGLTLLDDEFNMSVTRSNLSRRDPPPPARARQENMPPEE 120  
  
QY 121 PATTARGGPGKAGSRGFRAGHSEAGGSDRRRAGPEKPKSSRSGSGPQESSRDKRPL 180  
Db 121 RAAPARMADPKAGSRARATGHSEAGSGDRRRVGPEKPKSSRSGSGPQESSRDKRPL 180  
  
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHPHDVAPNGPSAGGLAIP 240  
Db 181 SGPDVSTTPQGSLSGTKLAAGRPNTPYPRADTDHPPRGAQGEHPHTMAPNGPSATGLAIP 240  
  
QY 241 QSSSSSRPPTTRAGAPSPGVLGPHASEPQLAPPA---CTPAAPAVPGPPGPRSPQREBPQ 297  
Db 241 Q---SSSSSRPPTTRAGAPSPGVLGPHASEPQLAPPA---CTPAAPAVPGPPGPRSPQREBPQ 299  
  
QY 298 RVSHQFRAALQLVDPGPRSYLDFNFKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQ 357  
Db 300 RVSHQFRAALQLVDPGPRSYLDFNFKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQ 359  
  
QY 358 QRRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRNNEQI 417  
Db 360 QRRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRNNEQI 419  
  
QY 418 AAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGFCQAQVSKVEPRKSLVG 477  
Db 420 AAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGFCQAQVSKVEPRKSLVG 479  
  
QY 478 TPYMWAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYFNEPPLKAMQWIRDNLPPLKN 537  
Db 480 TPYMWAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYFNEPPLKAMQWIRDNLPPLKN 539  
  
QY 538 LHKVSPSLKGFLLRLVDRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
Db 540 LHKASPSLKGFLDLRLVDRDPAQRATAAELLKHPFLTKAGPPASIVPLMRQNRTR 593

## RESULT 2

Q80297 ID Q80297 PRELIMINARY; PRT; 593 AA.  
AC Q80297;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE P21-activated protein kinase 4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RC SEQUENCE FROM N.A.  
FP STRAIN=BAIB/C;  
FM MEDLINE=22526742; PubMed=12529371;

RESULT 3  
Q8N4EI

RA Lu Y., Pan Z.Z., Devaux Y., Ray P.;  
RT "p21-activated Protein Kinase 4 (PAK4) Interacts with the Keratinocyte  
RT Growth Factor Receptor and Participates in Keratinocyte Growth Factor-  
RT mediated inhibition of Oxidant-induced Cell Death.";  
RL J. Biol. Chem. 278:10374-10380 (2003).  
DR EMBL; AY217016; AAO61496.1; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000095; PAKbox/RhoBndng.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR Pfam; PF00786; PBD; 1.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00285; PBD; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR SMART; SM00219; TyRK; 1.  
DR PROSITE; PS0108; CRIB; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW Kinase.  
SQ SEQUENCE 593 AA; 64666 MW; D7B3BD36706BAF4 CRC64;  
  
Query Match 92.3%; Score 2853; DB 11; Length 593;  
Best Local Similarity 92.6%; Pred. No. 1.4e-190;  
Matches 550; Conservative 9; Mismatches 31; Indels 4; Gaps 2;  
  
QY 1 MFGKKKVEISAPNFEHRVHTGFDQHEQKFTGLPRQWSLIESARRPKPLVDPACIT 60  
Db 1 MFGKKKVEISAPNFEHRVHTGFDQHEQKFTGLPRQWSLIESARRPKPLVDPACIT 60  
  
QY 61 SIQGPACTIIVRGSKGAKDGLTLLDDEFNMSVTRSNLSRRDPPPPARARQENMPPEE 120  
Db 61 SIQGPACTIIVRGSKGAKDGLTLLDDEFNMSVTRSNLSRRDPPPPARARQENMPPEE 120  
  
QY 121 PATTARGGPGKAGSRGFRAGHSEAGGSDRRRAGPEKPKSSRSGSGPQESSRDKRPL 180  
Db 121 RAAPARMADPKAGSRARATGHSEAGSGDRRRVGPEKPKSSRSGSGPQESSRDKRPL 180  
  
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHPHDVAPNGPSAGGLAIP 240  
Db 181 SGPDVSTTPQGSLSGTKLAAGRPNTPYPRADTDHPPRGAQGEHPHTMAPNGPSATGLAIP 240  
  
QY 241 QSSSSSRPPTTRAGAPSPGVLGPHASEPQLAPPA---CTPAAPAVPGPPGPRSPQREBPQ 297  
Db 241 Q---SSSSSRPPTTRAGAPSPGVLGPHASEPQLAPPA---CTPAAPAVPGPPGPRSPQREBPQ 299  
  
QY 298 RVSHQFRAALQLVDPGPRSYLDFNFKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQ 357  
Db 300 RVSHQFRAALQLVDPGPRSYLDFNFKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQ 359  
  
QY 358 QRRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRNNEQI 417  
Db 360 QRRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGGALTDIVTHTRNNEQI 419  
  
QY 418 AAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGFCQAQVSKVEPRKSLVG 477  
Db 420 AAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGFCQAQVSKVEPRKSLVG 479  
  
QY 478 TPYMWAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYFNEPPLKAMQWIRDNLPPLKN 537  
Db 480 TPYMWAPELISRLPYGPEVDIWSLIGIMVEMVDGEPYFNEPPLKAMQWIRDNLPPLKN 539  
  
QY 538 LHKVSPSLKGFLLRLVDRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
Db 540 LHKASPSLKGFLDLRLVDRDPAQRATAAELLKHPFLTKAGPPASIVPLMRQNRTR 593

ID Q8NAE1 PRELIMINARY; PRT; 501 AA.  
 AC Q8NAE1;  
 DT 01-OCT-2002 (TREMELrel. 22, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Similar to RIKEN cDNA 5730488L07 gene.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034511; AAH34511.1; -.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferrase activity; IEA.  
 DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000095; PAKBox/RhoBndng.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00669; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; TYRKC; 1.  
 DR PROSITE; PS50108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase.  
 SQ SEQUENCE 501 AA; 54940 MW; 6EE6240ECB65E79D CRC64;

Query Match 82.8%; Score 2558; DB 4; Length 501;  
 Best Local Similarity 84.8%; Pred. No. 4.2e-170;  
 Matches 501; Conservative 0; Mismatches 0; Indels 90; Gaps 1;  
 QY 1 MFGKRRKRVEISAPSNFHRVHTGFQHEQKFTGLPRQMSLIEESARRPKPLVDPAICIT 60  
 DB 1 MFGKRRKRVEISAPSNFHRVHTGFQHEQKFTGLPRQMSLIEESARRPKPLVDPAICIT 60  
 QY 61 SIQPGAPKTVIRGSKGAKGALTLTLLDEFENMSVTRSNLSLRDSDPPPPARQENGMPPEE 120  
 DB 61 SIQPGAPKTVIRGSKGAKGALTLTLLDEFENMSVTRSNLSLRDSDPPPPARQENGMPPEE 120  
 QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPGQESSRDKRPL 180  
 DB 121 PATTARGGPGK----- 131  
 QY 181 SGPDVGTGPAGLAKGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240  
 DB 132 -----GEPHDVAPNGPSAGGLAIP 150  
 QY 241 QSSSSSRPPTARGAPSPGVLGPHASEPOLAPACTPAAPAVGPGPPSPQREPORVS 300  
 DB 151 QSSSSSRPPTARGAPSPGVLGPHASEPOLAPACTPAAPAVGPGPPSPQREPORVS 210  
 QY 301 HEQFRAALQAVDPGDRPSYLDNFIKIGESTGIVCIATVRSKGLVAVKMDLRKQORR 360  
 DB 211 HEQFRAALQAVDPGDRPSYLDNFIKIGESTGIVCIATVRSKGLVAVKMDLRKQORR 270  
 QY 361 ELLEFNEVIMRDYQHENVNMYNSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAV 420  
 DB 271 ELLEFNEVIMRDYQHENVNMYNSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAV 330  
 QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQVSKVEVPRKSLVGTPT 480  
 DB 331 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGFCQVSKVEVPRKSLVGTPT 390

QY 481 WWAPELISRLPYGPEVDIWSLGIWVIEVMDGEPYPVNEPPLKAMKQVIRDNLPPRLKNLHK 540  
 DB 391 WWAPELISRLPYGPEVDIWSLGIWVIEVMDGEPYPVNEPPLKAMKQVIRDNLPPRLKNLHK 450  
 QY 541 VSPSLKGLFDRLLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
 DB 451 VSPSLKGLFDRLLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 501  
 RESULT 4  
 Q9ULS8  
 ID Q9ULS8 PRELIMINARY; PRT; 467 AA.  
 AC Q9ULS8;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Hypothetical protein KIAA1142 (Fragment).  
 GN KIAA1142.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20039618; PubMed=10574461;  
 RA Hiroseawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;  
 RT "Characterization of cDNA clones selected by the Genemark analysis  
 from size-fractionated cDNA libraries from human brain.";  
 RL DNA Res. 6:329-336(1999).  
 DR EMBL; AB032968; BAA86456.1; -.  
 DR HSSP; Q63450; 1A06.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferrase activity; IEA.  
 DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000095; PAKBox/RhoBndng.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00669; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS50108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Hypothetical protein; ATP-binding; Transferase.  
 FT NON TER 1  
 SQ SEQUENCE 467 AA; 51464 MW; EC342B8F5C5E3940 CRC64;  
 Query Match 71.3%; Score 2202.5; DB 4; Length 467;  
 Best Local Similarity 74.1%; Pred. No. 2.3e-145;  
 Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;  
 QY 1 MFGKRRKRVEISAPSNFHRVHTGFQHEQKFTGLPRQMSLIEESARRPKPLVDPAICIT 60  
 DB 30 MFGKRRKRVEISAPSNFHRVHTGFQHEQKFTGLPRQMSLIEESARRPKPLVDPAICIT 89  
 QY 61 SIQPGAPKTVIRGSKGAKGALTLTLLDEFENMSVTRSNLSLRDSDPPPPARQENGMPPEE 120  
 DB 90 SIQPGAPK----- 97  
 QY 121 PATTARGGPGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGGPGQESSRDKRPL 180  
 DB 98 ----- 97  
 QY 181 SGPDVGTGPAGLAKGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240  
 DB 98 -----GEPHDVAPNGPSAGGLAIP 116  
 QY 241 QSSSSSRPPTARGAPSPGVLGPHASEPOLAPACTPAAPAVGPGPPSPQREPORVS 300

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Db 117 QSSSSSRPPTTRARGAPSGVLGPHASEPQLAPPACTPAAPAVPGPPRSPQRPQVRS 176
QY 301 HQFRAALQLVVDGDPGRSYLDFNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360
Db 177 HQFRAALQLVVDGDPGRSYLDFNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRR 236
QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420
Db 237 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 296
QY 421 CLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPT 480
Db 297 CLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPT 356
QY 481 WNAPELISRLPYGPEVDIWSLGIWIMVMDGPPYFNEPPLKAMKMWIRNLPRLKNLHK 540
Db 357 WNAPELISRLPYGPEVDIWSLGIWIMVMDGPPYFNEPPLKAMKMWIRNLPRLKNLHK 416
QY 541 VSPSLKGFLLRLLVDRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
Db 417 VSPSLKGFLLRLLVDRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 467

RESULT 5
Q8NDE3
ID Q8NDE3; PRELIMINARY; PRT; 483 AA.
AC Q8NDE3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (fragment).
GN DKFP547G182.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834236; CAD38914.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGAP.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
FT NON_TER
SQ SEQUENCE 483 AA; 52787 MW; 8976E3BF0B8818B6 CRC64;

Query Match 71.3%; Score 2202.5; DB 4; Length 483;
Best Local Similarity 74.1%; Pred. No. 2.4e-145;
Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;

QY 1 MFGKKRKEVTSAPSNFHRVHTGPDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60
Db 46 MFGKKRKEVTSAPSNFHRVHTGPDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 105
QY 61 SIQPGAPKTVIRGSGKADGALTLLDDEFENSVTRNSLRDSDPPPPARARQENGMPPEE 120

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Db 106 SIQPGAPK----- 113
QY 121 PATTARGGPGKAGSRGRFAGHSEAGGGGDRRRAGPEKPKSRREGSGGPGQESSRDKRPL 180
Db 114 ----- 113
QY 181 SGPDVGTTPQAGLASGAKLAAGRPNFTYPRADTDHPSRGAQGEPHDVAHPNGPSAGGLAIP 240
Db 114 -----GEPHDVAPNGPSAGGLAIP 132
QY 241 QSSSSSRPPTTRARGAPSGVLGPHASEPQLAPPACTPAAPAVPGPPRSPQRPQVRS 300
Db 133 QSSSSSRPPTTRARGAPSGVLGPHASEPQLAPPACTPAAPAVPGPPRSPQRPQVRS 192
QY 301 HQFRAALQLVVDGDPGRSYLDFNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRR 360
Db 193 HQFRAALQLVVDGDPGRSYLDFNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQRR 252
QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 420
Db 253 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAV 312
QY 421 CLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPT 480
Db 313 CLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPT 372
QY 481 WNAPELISRLPYGPEVDIWSLGIWIMVMDGPPYFNEPPLKAMKMWIRNLPRLKNLHK 540
Db 373 WNAPELISRLPYGPEVDIWSLGIWIMVMDGPPYFNEPPLKAMKMWIRNLPRLKNLHK 432
QY 541 VSPSLKGFLLRLLVDRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
Db 433 VSPSLKGFLLRLLVDRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 483

RESULT 6
Q90W62
ID Q90W62 PRELIMINARY; PRT; 650 AA.
AC Q90W62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PAK5 protein.
GN PAK5.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RA Cau J., Faure S., Delsert C., Morin N.;
RT "A novel xenopus p21 activated kinase expressed in brain.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277826; CAC40979.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGAP.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
KW ATP-binding; Transferase.

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SQ SEQUENCE 650 AA; 73736 MW; 9274DC6CACD4A081 CRC64;
Query Match 68.8%; Score 2124.5; DB 13; Length 650;
Best Local Similarity 66.4%; Pred. No. 9.5e-140;
Matches 442; Conservative 43; Mismatches 90; Indels 91; Gaps 13;
QY 1 MFGKKKVEISAPNFEHVRHTGDFDQEQKFTGLPRQWQSILIESARRPKPLVDPAICIT 60
DB 1 MFAKKKVEISAPNFEHVRHTGDFDQEQKFTGLPRQWQSILIESARRPKPLVDPSVIT 60
QY 61 STQPGAPKTIVRGSKGAKDGLTLLDEFENMSVTRSNLSLRDSP---PPPARAQENGM 117
DB 61 TIKHVPQKTIVRGNKSLDGLSLAWLLDEFDDMSVCKSNLSLRSPPCOPREGRFHQENGM 120
QY 118 PB-----EPATTARGG----- 128
DB 121 SEVRVROQREDQGRSENRSEHRRERQREHRAVPOQPGOEFSNKHRRPPPPYPKDI 180
QY 129 PGKAGSRGRFAGHSBAGG-----GSGD-----RRRAGPEKRPKSS-REGSGGPOE 172
DB 181 PEKRGPR-----SHEKSDGERREYPGNDRGHSDPVERVVKDKGEEKPKSAVTSGESGPQ- 235
QY 173 SSRDKRPLSGPDVGPQTPAGLASGAK-LAAGRPENTYPRADTDHPSRGAGQEPHDVAPNG 231
DB 236 SPRDKRPLSGPNIRTPGSSSTDGVVKQTETGRPFNTYPRATD-DNRGAHQVSDSRSTV 294
QY 232 P-----SAGGLAIQSSSSSRPPTARGAPSPGVLGPHASEPOLAPACTPAAPAVPG 285
DB 295 PLDSKSSVSKGSSRPQGGQVKKPPEK-----PHPTQLAPHSSDPQLSRPVQT-----QH 344
QY 286 PPGPSPQEPQVRSHEQFRAALQLVDPGDRPSYLDNFIKIGEGSTGIVCIATVRSSGK 345
DB 345 PAQPSQPQEPQVRSHEQFRAALQVDPGDRPTLDNFIKIGEGSTGIVCIATIKSSGK 404
QY 346 LVAVKMDLRKQORRELLFNEVVIWRDYQHENVVEMNSYLVGDELWVWMEFEGGALTD 405
DB 405 LVAVKMDLRKQORRELLFNEVVIWRDYQHENVVEMNSYLVGDELWVWMEFEGGALTD 464
QY 406 IVTHTRMNEEQIAANCLAVLQALSVLHAQGVHTRDKSDSILLTHDGRVKLSDFGFCACV 465
DB 465 IVTHTRMNEEQIATCVSVLKALSVLHAQGVHTRDKSDSILLTHDGRVKLSDFGFCACV 524
QY 466 SKEVPRKSLVGTTPYMAPELISRLPYGPEVDIWSLGIWVEMVDCGEPYFNEPPLKAMK 525
DB 525 NKEVPRKSLVGTTPYMAPELISRLPYGPEVDIWSLGIWVEMVDCGEPYFNEPPLKAMK 584
QY 526 MTRDNLPPRLKXNKHVSPSLKGLFDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLM 585
DB 585 MTRDNLPPRLKXNAQKVSPLLKGLFDRLLVRDPSQASANELLKHPFLGKAGPPSCIVPLM 644
QY 586 QNRNTR 591
DB 645 QNRNMR 650
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RESULT 7
Q8K0U2 PRELIMINARY; PRT; 407 AA.
ID Q8K0U2
AC Q8K0U2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN PAK4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA Strausberg R.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL
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DR EMBL; BC030389; AAH30389.1; -.
DR MGI; 1917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 407 AA; 44339 MW; 921689734DF9D710 CRC64;
Query Match 63.7%; Score 1967; DB 11; Length 407;
Best Local Similarity 94.5%; Pred. No. 5e-129;
Matches 380; Conservative 5; Mismatches 13; Indels 4; Gaps 2;
QY 193 LASGAKLAAGRPENTYPRADTDHPSRGAGQEPHDVAPNGSPSAGGLAIQSSSSSRPPTR 252
DB 7 LTSGLTKLAAGRPENTYPRADTDHPSRGAGQEPHDVAPNGSPSATGLAAPQ-SSSSSRPPTR 65
QY 253 ARGAPSPGVLGPHASEPOLAPPA---CTPAAPAVPGPGRSPQEPQVRSHEQFRAALQ 309
DB 66 ARGAPSPGVLGPHASEPOLAPPAALAAPAVPAPGPPGPRSPQEPQVRSHEQFRAALQ 125
QY 310 LVVDPGDRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVI 369
DB 126 LVVDPGDRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVI 185
QY 370 MRDYQHENVVEMNSYLVGDELWVWMEFEGGALTDIVTHTRMNEEQIAANCLAVLQALS 429
DB 186 MRDYQHENVVEMNSYLVGDELWVWMEFEGGALTDIVTHTRMNEEQIAANCLAVLQALS 245
QY 430 VLHAQGVHTRDKSDSILLTHDGRVKLSDFGFCACVSKVPRKSLVGTTPYMAPELISR 489
DB 246 VLHAQGVHTRDKSDSILLTHDGRVKLSDFGFCACVSKVPRKSLVGTTPYMAPELISR 305
QY 490 LPYGPEVDIWSLGIWVEMVDCGEPYFNEPPLKAMKMRDNLPPRLKXNKHVSPSLKGLF 549
DB 306 LPYGPEVDIWSLGIWVEMVDCGEPYFNEPPLKAMKMRDNLPPRLKXNKHVSPSLKGLF 365
QY 550 DRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 366 DRLLVRDPAQRATAAELLKHPFLTKAGPPASIVPLMRQNRTR 407
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RESULT 8
Q8C015 PRELIMINARY; PRT; 719 AA.
ID Q8C015
AC Q8C015;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine-protein kinase PAK 5.
GN 2900083L08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
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[illegible]





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Db 391 GQVAVKMDLRKQORRELLFNEVIMRDYHHNIVETYSYFLVNDLWVWVYLEGGAL 450
QY 404 TDIVTHTRMNEEQIAAVCLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCA 463
Db 451 TDIVTHSRMDEEQIATVCKQCKALAYLHSCQVHHRDIKSDSILLAAADGRVKLSDFGCA 510
QY 464 QVSKVEPRKSLVGTGYMMAPELISRLPYGPEVDIWSLGIWVMDGEPYFNEPPLKA 523
Db 511 QVSKVEPRKSLVGTGYMMAPELISRLPYGPEVDIWSLGIWVMDGEPYFNEPPLQA 570
QY 524 MKMIRDNLPPRLKNLHKVSPSLKGFLLVRDPAQRATAAELLKHPFLAKAGPPASIVP 583
Db 571 MRRIIDMQPPLKNAHKVSPRLQSFLLRMLVRDPAQRATAAELLKHPFLAKAGPPSLVLP 630
QY 584 LMRQNR 589
Db 631 LMRNAR 636

RESULT 12
Q960J8 PRELIMINARY; PRT; 639 AA.
AC Q960J8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LD47563p.
GN MBLT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STAPLETON M., BROKSTEIN P., HONG L., AGBAYANI A., CARLSON J.,
RA CHAMPE M., CHAVEZ C., DORSETT V., FARFAN D., FRISE E., GEORGE R.,
RA GONZALEZ M., GUARIN H., LI P., LIAO G., MIRANDA A., MUNGALL C.J.,
RA NUNO J., FACIEB J., PARAGAS V., PARK S., PHOUANAVONG S., WAN K.,
RA YU C., LEWIS S.E., RUBIN G.M., CELNIKER S.
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052023; AAK93447.1; -
DR HSSP; P24941; 1BUH.
DR Flybase; FBgn0025743; mbl.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndg.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PKB; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PKB; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 639 AA; 69592 MW; 2145317F0A89F554 CRC64;

Query Match 48.5%; Score 1497.5; DB 5; Length 639;
Best Local Similarity 50.3%; Pred. No. 4.7e-96;
Matches 335; Conservative 65; Mismatches 159; Indels 107; Gaps 13;

QY 1 MFGKRRKRVRISAPNPEHRVHTGFDQHEQKFTGLPRQWQL-----IEESARRPKPLVD 55
Db 1 MFSKKKKPLISMESNPEHRVHTGFDKREKNTYVGLPLQWASIVGNQILKSSNRPLPLVD 60
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QY 56 PACITSIQGPAPKTIVR-----GSKGAKDGAALTLLLDDEFENMS----- 93
Db 61 PSEITPTFILLDLKTIIVRPHNNKADTTLSNSSSTMMGSMAPNMPMAPGAHPMMHSGPG 120
QY 94 -----VTRNSLRSDSPPPAR-AROENGMPEEPATARGGPGKAG-S 134
Db 121 MMPPETGGIVLPKTSHVARSNSLRSSSPVRRVRYANVPSPVEEGPFAAGTFCVGCGAS 180
QY 135 RGRF-----AGHSEAGGSGDRRAGPEKPKRSREGSGGQESRRDKRPLSG 182
Db 181 SGGFKPGAHPSLLYNSQAHANGATG-----PLAVRTDQTNLQVRSNLIAPSSG 230
QY 183 PDVGTPTPAGLASGAKLAAGRPFTNYPRADTHPSRGAQGEPHDVAPNGPSAGGL--AIP 240
Db 231 GSM--PQQQQTSPVGSVASGTRSN-----HSHNTNNGNSGSGYPPMVP 270
QY 241 QSSSSSSRPPTRAR--GAPSPGVLGPH-----ASEPQLAPPACTPAAPVP 284
Db 271 TSHQQQQQQQQQAQKQGDQGNQNLPHPHHQLAKSASRASSSSGGASAAQQAAS 330
QY 285 GPPGPRSPQ-REPQSVSHQFRAALQVLVVDGDRSYLDNFIKIGEGSTGIVCIATVRSS 343
Db 331 GASGGAAGQPKQDQRLTHEQFRAALQMVVSAGDPRENLDHFNKIGEGSTGIVCIATDKST 390
QY 344 GKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVWVMEFLEGGAL 403
Db 391 GQVAVKMDLRKQORRELLFNEVIMRDYHHNIVETYSYFLVNDLWVWVYLEGGAL 450
QY 404 TDIVTHTRMNEEQIAAVCLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCA 463
Db 451 TDIVTHSRMDEEQIATVCKQCKALAYLHSCQVHHRDIKSDSILLAAADGRVKLSDFGCA 510
QY 464 QVSKVEPRKSLVGTGYMMAPELISRLPYGPEVDIWSLGIWVMDGEPYFNEPPLKA 523
Db 511 QVSKVEPRKSLVGTGYMMAPELISRLPYGPEVDIWSLGIWVMDGEPYFNEPPLQA 570
QY 524 MKMIRDNLPPRLKNLHKVSPSLKGFLLVRDPAQRATAAELLKHPFLAKAGPPASIVP 583
Db 571 MRRIIDMQPPLKNAHKVSPRLQSFLLRMLVRDPAQRATAAELLKHPFLAKAGPPSLVLP 630
QY 584 LMRQNR 589
Db 631 LMRNAR 636

RESULT 13
O96372 PRELIMINARY; PRT; 639 AA.
AC O96372;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE STE20 serine/threonine protein kinase homolog.
GN MBLT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Melnick M.B.;
RT "New Drosophila member of the Ste20 serine/threonine kinase family.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031517; AAD01935.1; -.
DR HSSP; P24941; 1BUH.
DR FlyBase; FBgn0025743; mbl.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK017713; BAB30889.1; -.  
 DR HSSP; Q63450; IA06.  
 DR MGD; MGI:1917834; Pak4.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.  
 FT NON\_TER 1  
 SQ SEQUENCE 229 AA; 25896 MW; D9CF2CA73CED941E CRC64;

Query Match 37.5%; Score 1160; DB 11; Length 229;  
 Best Local Similarity 96.9%; Pred. No. 4.2e-73;  
 Matches 222; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 363 LFNEVVIMRDYQHENVVEMYSYINGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAVCL 422  
 Db 1 LFNEVVIMRDYRHENVVEMYSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAVCL 60  
 QY 423 AVLQALSVLHAQGVIIHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPLYWM 482  
 Db 61 AVLQALAVLHAQGVIIHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPLYWM 120  
 QY 483 APELISRLPYGPEVDIWSLGIWVIEVDGPPYFNEPPLKAMKMWIRDLNLPRLKNLHKVS 542  
 Db 121 APELISRLPYGPEVDIWSLGIWVIEVDGPPYFNEPPLKAMKMWIRDLNLPRLKNLHKAS 180  
 QY 543 PSLKGFDLRLVDRDPQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
 Db 181 PSLKGFDLRLVDRDPQRAPAAELLKHPFLTKAGPPASIVPLMRQNRTR 229

Search completed: September 29, 2004, 18:04:41  
 Job time : 138.844 secs

B/gnK

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: September 29, 2004, 17:36:56 ; Search time 154.703 Seconds  
(without alignments)  
1079.395 Million cell updates/sec

Title: US-10-693-367-2  
Perfect score: 3090  
Sequence: 1 MFGKKRKYEISAPSNFHR.....LAKAGPPASIVPLMRQNR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3090	100.0	591	2	AAY55964 Full leng
2	3090	100.0	591	3	AAY59128 Human ser
3	3090	100.0	591	7	ADC37307 Nuclear f
4	3090	100.0	591	7	ADD89973 Human can
5	3090	100.0	620	4	ABG19308 Novel hum
6	2558	82.8	501	7	ADC37309 Nuclear f
7	2202.5	71.3	438	7	ADC37305 Nuclear f
8	2073	67.1	398	2	AAY55941 Human PAK
9	1734	56.1	719	4	AAM38963 Human pol
10	1731	56.0	719	4	AAB65705 Novel pro
11	1731	56.0	719	7	ADC37451 Nuclear f
12	1730	56.0	719	4	AEO2187 Human p21
13	1502	48.6	293	7	ADL15851 PAK4KD pr
14	1473.5	47.7	681	2	AAY55940 Human PAK
15	1473.5	47.7	681	3	AAB03967 Signal tr
16	1473.5	47.7	681	4	AAB20337 Human PAK
17	1473.5	47.7	681	5	ABP64709 Human pro
18	1473.5	47.7	701	6	ABU11508 Human MDD
19	1470.5	47.6	681	3	AAB03970 Mutant si
20	1470.5	47.6	681	4	AAG63230 Amino aci
21	1448.5	46.9	681	3	AAB03971 Mutant si
22	1335.5	43.2	641	5	AAE16269 Human kin
23	1277	41.3	250	3	AAY59129 Human PAK
24	1251.5	40.5	632	4	AAB85788 Human kin
25	1244.5	40.3	547	4	AAG67825 Human P21

## ALIGNMENTS

RESULT 1  
AAY55964  
ID AAY55964 standard; protein; 591 AA.

XX AAY55964;

XX AC

XX 18-FEB-2000 (first entry)

XX Full length human PAK5 protein.

XX DE

XX Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;  
KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;  
KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;  
KW vulnery; STE20; protein kinase; STIK2; STIK3; STIK4; STIK5; STIK6; STIK7;  
ZC1; ZC2; ZC3; ZC4; RKS2; SULU3; SULU2; STIK4; STIK5; STIK6; STIK7;  
KW antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;  
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
KW myocardial infarction; cardiovascular disease; stroke; renal failure;  
KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
KW mesangial disorder; growth regulation; wound healing; T cell activation;  
KW immunosuppressant.

XX Homo sapiens.

XX MO9953036-A2.

XX 21-OCT-1999.

XX 13-APR-1999; 99WO-US008150.

XX 14-APR-1998; 98US-0081784P.

XX (SUGS-) SUGEN INC.

XX Plowman G, Martinez R, Whyte D;

XX WPI; 1999-611301/52.

XX N-PSDB; AA240538.

XX Novel kinase-related polypeptides used for the diagnosis and treatment of

XX kinase-related diseases and disorders.

XX Claim 11; Page 366-368; 387pp; English.

XX This sequence represents a novel STE20-related protein kinase. The

CC invention relates to nucleic acid molecule encoding a kinase polypeptide  
 CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,  
 CC ZC4, XBS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to  
 CC identify agonists and antagonists, and to raise antibodies. The  
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,  
 CC polypeptides, antibodies, antagonists and agonists may be used to treat  
 CC diseases such as immune-related disorders and diseases (e.g. rheumatoid  
 CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.  
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,  
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory  
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial  
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative  
 CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral  
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,  
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes  
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be  
 CC useful for cell growth regulation (e.g. in wound healing), T cell  
 CC activation, mitosis control, and as immunosuppressants  
 XX  
 SQ Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 2; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-216; Indels 0; Gaps 0;  
 Matches 591; Conservative 0; Mismatches 0;  
 QY 1 MFGKKKRVETISAPNFEHRVHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60  
 DB 1 MFGKKKRVETISAPNFEHRVHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60  
 QY 61 SIQGPAPKTIIVRGSGAKDGALTLLDEFENSVTRNSLRDSDPPPPARARQENGMPEE 120  
 DB 61 SIQGPAPKTIIVRGSGAKDGALTLLDEFENSVTRNSLRDSDPPPPARARQENGMPEE 120  
 QY 121 PATTARGGPKAGSGRAGHSEAGGSDRRRAGPEKPKSRREGSGGPQSSRDKRLP 180  
 DB 121 PATTARGGPKAGSGRAGHSEAGGSDRRRAGPEKPKSRREGSGGPQSSRDKRLP 180  
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240  
 DB 181 SGPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240  
 QY 241 QSSSSSSRPPTARGAPSPGVLGPASEPQLAPPACTPAAPVPGPPRSPQRPQVRS 300  
 DB 241 QSSSSSSRPPTARGAPSPGVLGPASEPQLAPPACTPAAPVPGPPRSPQRPQVRS 300  
 QY 301 HEQFRAALQLVVDPGDPRSYLDFNFIKIGEGSTGIVCIATVRSGLKLVAVKMDLRKQRR 360  
 DB 301 HEQFRAALQLVVDPGDPRSYLDFNFIKIGEGSTGIVCIATVRSGLKLVAVKMDLRKQRR 360  
 QY 361 ELLFNEVIMRDYQHENVVEMYSYLVGDDELWMVMEFLEGGALTDTIVTRNNEEQIAAV 420  
 DB 361 ELLFNEVIMRDYQHENVVEMYSYLVGDDELWMVMEFLEGGALTDTIVTRNNEEQIAAV 420  
 QY 421 CLAVLQALSVLHAQGVIRHDIKSDSLITLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480  
 DB 421 CLAVLQALSVLHAQGVIRHDIKSDSLITLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480  
 QY 481 WNAPELISRLPYGPEVDIWSLGIWTEVDGPPYFNEPPLKAMKIRNLPRLKNLHK 540  
 DB 481 WNAPELISRLPYGPEVDIWSLGIWTEVDGPPYFNEPPLKAMKIRNLPRLKNLHK 540  
 QY 541 VSPSLKGFGLDRLLVRDPAQATAAELLKHFFLAKAGPPASIVPLMRQNRTR 591  
 DB 541 VSPSLKGFGLDRLLVRDPAQATAAELLKHFFLAKAGPPASIVPLMRQNRTR 591

RESULT 2

AA59128

ID AA59128 standard; protein; 591 AA.

XX

AC AA59128;

XX

DT 08-MAR-2000 (first entry)

XX Human serine/threonine kinase, PAK4.  
 DE  
 XX PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;  
 XX Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human;  
 KW actin polymerization; filopodia; cancer; arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9963073-A1.  
 PN  
 XX 09-DEC-1999.  
 PD  
 XX  
 XX 21-MAY-1999; 99WO-US011341.  
 PF  
 XX 21-MAY-1998; 98US-00082737.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX Minden A;  
 PI  
 XX  
 XX WPI: 2000-072881/06.  
 DR  
 XX N-PSDB; AAZ40857.  
 DR  
 XX Novel mammalian nucleic acid useful for treating cancer and arthritis.  
 PT  
 XX Claim 8; Fig 1A-B; 95pp; English.  
 PS  
 XX The invention relates to an isolated mammalian nucleic acid that encodes  
 CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an  
 CC effector for the GTPases Rac and Cdc42Hs which are involved in  
 CC intracellular signal cascades, morphogenesis and mitogenesis, and  
 CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of  
 CC PAK4 with these enzymes will thus result in inhibition of actin  
 CC polymerization and formation of filopodia. The PAK4 nucleic acid used for  
 CC recombinant production of the protein, and as a source of probes for  
 CC identifying homologous sequences and of (anti)sense oligonucleotides for  
 CC inhibiting PAK4 expression. The protein, or its fragments, are used to  
 CC raise specific antibodies and these are useful as ligands for therapeutic  
 CC inhibition of interaction between PAK4 and its native binding partners.  
 CC Inhibition of PAK4 activity or expression is used for treatment of cancer  
 CC and arthritis. The present sequence represents the human serine/threonine  
 CC kinase, PAK4  
 CC  
 SQ Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 3; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-216; Indels 0; Gaps 0;  
 Matches 591; Conservative 0; Mismatches 0;  
 QY 1 MFGKKKRVETISAPNFEHRVHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60  
 DB 1 MFGKKKRVETISAPNFEHRVHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACIT 60  
 QY 61 SIQGPAPKTIIVRGSGAKDGALTLLDEFENSVTRNSLRDSDPPPPARARQENGMPEE 120  
 DB 61 SIQGPAPKTIIVRGSGAKDGALTLLDEFENSVTRNSLRDSDPPPPARARQENGMPEE 120  
 QY 121 PATTARGGPKAGSGRAGHSEAGGSDRRRAGPEKPKSRREGSGGPQSSRDKRLP 180  
 DB 121 PATTARGGPKAGSGRAGHSEAGGSDRRRAGPEKPKSRREGSGGPQSSRDKRLP 180  
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240  
 DB 181 SGPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGSAGGLAIP 240  
 QY 241 QSSSSSSRPPTARGAPSPGVLGPASEPQLAPPACTPAAPVPGPPRSPQRPQVRS 300  
 DB 241 QSSSSSSRPPTARGAPSPGVLGPASEPQLAPPACTPAAPVPGPPRSPQRPQVRS 300  
 QY 301 HEQFRAALQLVVDPGDPRSYLDFNFIKIGEGSTGIVCIATVRSGLKLVAVKMDLRKQRR 360  
 DB 301 HEQFRAALQLVVDPGDPRSYLDFNFIKIGEGSTGIVCIATVRSGLKLVAVKMDLRKQRR 360

QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAV 420  
 DB 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAV 420  
 QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEVPRKSLVGTPT 480  
 DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEVPRKSLVGTPT 480  
 QY 481 WMAPELISRLPYGPEVDIWSLGIWVMEVDGEPYPNEPPLKAMKMIKMDLPPRLKXHLK 540  
 DB 481 WMAPELISRLPYGPEVDIWSLGIWVMEVDGEPYPNEPPLKAMKMIKMDLPPRLKXHLK 540  
 QY 541 VPSLKGFLDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
 DB 541 VPSLKGFLDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 3  
 ADC37307  
 ID ADC37307 standard; protein; 591 AA.  
 XX  
 AC ADC37307;  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 140.  
 XX  
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;  
 KW cancer; infectious disease; bone disease; AIDS;  
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;  
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;  
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003048202-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 03-DEC-2002; 2002WO-JP012644.  
 XX  
 PR 03-DEC-2001; 2001JP-00368692.  
 PR 05-DEC-2001; 2001US-0335829P.  
 PR 03-OCT-2002; 2002JP-00291302.  
 PR 04-OCT-2002; 2002US-0415769P.  
 XX  
 PA (ASAH ) ASahi KASEI KK.  
 XX  
 PI Matsuda A, Muramatsu S;  
 XX  
 DR WPI: 2003-505282/47.  
 DR N-PSDB; ADC37306.  
 XX  
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),  
 PT useful for treating inflammation, autoimmune diseases, cancers,  
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or  
 PT ischemic disorders.  
 XX  
 PS Claim 1; SEQ ID NO 140; 938pp; English.  
 XX  
 CC The present invention relates to novel proteins and their coding  
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-  
 CC kappaB). The proteins and their coding sequences are useful for treating  
 CC a disease associated with NF-kappaB activation, such as inflammation,  
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,  
 CC neurodegenerative diseases, or ischaemic disorders.  
 XX  
 SQ Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 7; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-216;  
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCKRKKRVEISAPSNFHRVHTGFDQHEQKFTGLPRQWQSLLIESARBRKPLVDPAKIT 60  
 DB 1 MFCKRKKRVEISAPSNFHRVHTGFDQHEQKFTGLPRQWQSLLIESARBRKPLVDPAKIT 60  
 QY 61 STQPGAPKTIIVRGSKGAKDQALTLTLLDEFENSVTRSNLSLRDSDPPPARARQENGWPEE 120  
 DB 61 STQPGAPKTIIVRGSKGAKDQALTLTLLDEFENSVTRSNLSLRDSDPPPARARQENGWPEE 120  
 QY 121 PATTARGGKAGSRORFAGHSEAGGSGDRRRRAGPEKPKSKSREGSGGPFQESSRDKRPL 180  
 DB 121 PATTARGGKAGSRORFAGHSEAGGSGDRRRRAGPEKPKSKSREGSGGPFQESSRDKRPL 180  
 QY 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIP 240  
 DB 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIP 240  
 QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPRSPQREPORVS 300  
 DB 241 QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPRSPQREPORVS 300  
 QY 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSGLVAVKXMDLRKQRR 360  
 DB 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSGLVAVKXMDLRKQRR 360  
 QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAV 420  
 DB 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLEGALTDIVTHRMNEEQIAAV 420  
 QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEVPRKSLVGTPT 480  
 DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEVPRKSLVGTPT 480  
 QY 481 WMAPELISRLPYGPEVDIWSLGIWVMEVDGEPYPNEPPLKAMKMIKMDLPPRLKXHLK 540  
 DB 481 WMAPELISRLPYGPEVDIWSLGIWVMEVDGEPYPNEPPLKAMKMIKMDLPPRLKXHLK 540  
 QY 541 VPSLKGFLDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
 DB 541 VPSLKGFLDRLVLRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 4  
 ADD89973  
 ID ADD89973 standard; protein; 591 AA.  
 XX  
 AC ADD89973;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human cancer-associated protein kinase PAK4.  
 XX  
 KW PAK4; protein kinase; enzyme; cancer; cytostatic; immunosuppressive;  
 KW antidiabetic; antirheumatic; antiarthritic; antipsoriatic;  
 KW antiangiogenic; antiarteriosclerotic; antiinflammatory; vulnery;  
 KW gynaecological; neuroprotective; gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003083096-A2.  
 XX  
 PD 09-OCT-2003.  
 XX  
 PF 21-MAR-2003; 2003WO-CA000409.  
 XX  
 PR 28-MAR-2002; 2002US-0368853P.  
 XX  
 PA (KINE-) KINETEK PHARM INC.  
 XX  
 PI Delaney AD;  
 XX  
 DR WPI; 2003-833542/77.  
 DR N-PSDB; ADD89972.

XX New nucleic acids encoding cancer associated protein kinases, useful as  
PT targets for screening pharmaceutical agents that inhibit the growth of  
PT tumor cells, or for diagnosing and treating cancer, inflammation or  
XX autoimmune disease.  
XX  
XX Claim 1; Page 77-78; 91pp; English.  
XX  
XX The present sequence is the protein sequence of human cancer-associated  
CC protein kinase, PAK4. PAK-related kinase PAK4 is an effector molecule for  
CC Cdc42hs. Its gene expression is up-regulated in cancers of the brain,  
CC lung, muscle and uterus. PAK4 is one of a set of protein kinases that are  
CC shown by the invention to be over-expressed in hyper-proliferative cells.  
XX These protein kinases provide targets for drug screening for agents  
CC effective in inhibiting the growth or metastasis of tumour cells, and for  
CC determining other molecular targets in kinase signal transduction  
CC pathways involved in transformation and growth of tumour cells. A claimed  
CC method for inhibiting the growth of a cancer cell involves down-  
CC regulating the activity of the protein kinase using an antisense sequence  
CC or inhibitor of kinase activity, especially where the cancer cell is a  
CC breast, liver, colon, muscle, prostate, kidney, lung, placental or  
CC uterine cancer cell. Detection of over-expression in cancers provides a  
CC useful diagnostic for predicting patient prognosis and probability of  
CC drug effectiveness. Agents that specifically bind the protein kinases can  
CC be used for treatment and visualisation of tumours in patients. The  
CC protein kinase polypeptides and nucleic acids may also be used for  
CC treating hyperproliferative diseases, such as autoimmune disease,  
CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis,  
CC atherosclerosis, inflammation, scarring, endometriosis and angiogenesis.  
XX  
XX Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 7; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.3e-216;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWQSLIESARRPKPLVDPA 60  
Db 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWQSLIESARRPKPLVDPA 60  
QY 61 STQPGAPKTVIRGSKAKGALVTLTLLDEFENMSVTRNSLRDSDPPPPARARQENMP 120  
Db 61 STQPGAPKTVIRGSKAKGALVTLTLLDEFENMSVTRNSLRDSDPPPPARARQENMP 120  
QY 121 PATTARGGPKAGSRGFRAGHSAGGSDRRRAGPEKPKSRREGSGGPGQSSRRKRL 180  
Db 121 PATTARGGPKAGSRGFRAGHSAGGSDRRRAGPEKPKSRREGSGGPGQSSRRKRL 180  
QY 181 SGPDVGTPOQAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAENGPSAGGLA 240  
Db 181 SGPDVGTPOQAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAENGPSAGGLA 240  
QY 241 QSSSSSRPPTARGAPSGVLGPHASEPOLAPACTPAAPVGGPGPRSPQREPORVS 300  
Db 241 QSSSSSRPPTARGAPSGVLGPHASEPOLAPACTPAAPVGGPGPRSPQREPORVS 300  
QY 301 HQQFRAALQVDPGPRSLDNFIKIGSGTGIVCIATVRSGKLVAVKMDLRKQORR 360  
Db 301 HQQFRAALQVDPGPRSLDNFIKIGSGTGIVCIATVRSGKLVAVKMDLRKQORR 360  
QY 361 ELLFNEVIMRDIYQHENVEMVNSYLVGDELVWVMEFLEGGALTDIVTTRMNEEQIAAV 420  
Db 361 ELLFNEVIMRDIYQHENVEMVNSYLVGDELVWVMEFLEGGALTDIVTTRMNEEQIAAV 420  
QY 421 CLAVLOALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGT 480  
Db 421 CLAVLOALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLVGT 480  
QY 481 WNAPELISRLPYGPEVDINSLGIWVEMVDGEPYFNEPPLKAMKIMRDNLPRLKNLHK 540  
Db 481 WNAPELISRLPYGPEVDINSLGIWVEMVDGEPYFNEPPLKAMKIMRDNLPRLKNLHK 540  
QY 541 VPSLKGFLDRLLRVDPQAORATAAELLKHFPFLAKAGPPASIVPLMRQNRTR 591

Db 541 VPSLKGFLDRLLRVDPQAORATAAELLKHFPFLAKAGPPASIVPLMRQNRTR 591  
RESULT 5  
ABG19308  
ID ABG19308 standard; protein; 620 AA.  
XX AC ABG19308;  
XX AC ABG19308;  
DT 18-FEB-2002 (first entry)  
DE Novel human diagnostic protein #19299.  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX Homo sapiens.  
XX WO200175067-A2.  
PD 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS83495.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 20; SEQ ID NO 49667; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have application in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 620 AA;  
Query Match 100.0%; Score 3090; DB 4; Length 620;  
Best Local Similarity 100.0%; Pred. No. 2.5e-216;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWQSLIESARRPKPLVDPA 60  
Db 30 MFGKKRKRVEISAPSNFHRVHTGPDQHEQKFTGLPRQWQSLIESARRPKPLVDPA 89

QY 61 SIQGAPKTIVRGSKGAKDGLTLLDDEPNMVSRTSNLSRRDPPPPAPARQENGMPPE 120  
 DB 90 SIQGAPKTIVRGSKGAKDGLTLLDDEPNMVSRTSNLSRRDPPPPAPARQENGMPPE 149  
 QY 121 PATTARGGPKAGSRGRFAGHSAGGSGDRRRAGPEKRPKSSREGSGGQESSRDKRPL 180  
 DB 150 PATTARGGPKAGSRGRFAGHSAGGSGDRRRAGPEKRPKSSREGSGGQESSRDKRPL 209  
 QY 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQEPHDVAPNGPSAGGLAIP 240  
 DB 210 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQEPHDVAPNGPSAGGLAIP 269  
 QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGPRSPQREPORVS 300  
 DB 270 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGPRSPQREPORVS 329  
 QY 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSRGKLVAVKMDLRKQORR 360  
 DB 330 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSRGKLVAVKMDLRKQORR 389  
 QY 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGALTIDIVTHRMNEEQIAAV 420  
 DB 390 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGALTIDIVTHRMNEEQIAAV 449  
 QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTTPY 480  
 DB 450 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTTPY 509  
 QY 481 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNEPPLKAMKIMIRNDLPPRLKNLHK 540  
 DB 510 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNEPPLKAMKIMIRNDLPPRLKNLHK 569  
 QY 541 VPSLKGFLDRLVDRPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
 DB 570 VPSLKGFLDRLVDRPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 620

RESULT 6  
 ADC37309  
 ID ADC37309 standard; protein; 501 AA.  
 XX ADC37309;  
 AC  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 142.  
 XX  
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;  
 KW cancer; infectious disease; bone disease; AIDS;  
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;  
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;  
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003048202-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 03-DEC-2002; 2002WO-JP012644.  
 XX  
 PR 03-DEC-2001; 2001JP-00368692.  
 PR 05-DEC-2001; 2001US-0335829P.  
 PR 03-OCT-2002; 2002JP-00291302.  
 PR 04-OCT-2002; 2002US-0415769P.  
 XX  
 XX (ASAH ) ASAH KASEI KK.  
 XX  
 XX Matsuda A, Muramatsu S;  
 PI  
 XX WPI; 2003-505282/47.  
 DR N-PSDB; ADC37308.

XX New purified protein that activates nuclear factor kappa B (NF-kappaB),  
 PT useful for treating inflammation, autoimmune diseases, cancers,  
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or  
 PT ischemic disorders.  
 XX  
 PS Claim 1; SEQ ID NO 142; 938pp; English.  
 XX  
 CC The present invention relates to novel proteins and their coding  
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-  
 CC kappaB). The proteins and their coding sequences are useful for treating  
 CC a disease associated with NF-kappaB activation, such as inflammation,  
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,  
 CC neurodegenerative diseases, or ischaemic disorders.  
 XX  
 SQ Sequence 501 AA;

Query Match 82.8%; Score 2558; DB 7; Length 501;  
 Best Local Similarity 84.8%; Pred. No. 1e-177;  
 Matches 501; Conservative 0; Mismatches 0; Indels 90; Gaps 1;  
 QY 1 MFGRKRVVEISAPSNFEHRVHTGPDQHQKFTGLPRQWSLIEESARRPKPLVDPAKIT 60  
 DB 1 MFGRKRVVEISAPSNFEHRVHTGPDQHQKFTGLPRQWSLIEESARRPKPLVDPAKIT 60  
 QY 61 SIQGAPKTIVRGSKGAKDGLTLLDDEPNMVSRTSNLSRRDPPPPAPARQENGMPPE 120  
 DB 61 SIQGAPKTIVRGSKGAKDGLTLLDDEPNMVSRTSNLSRRDPPPPAPARQENGMPPE 120  
 QY 121 PATTARGGPKAGSRGRFAGHSAGGSGDRRRAGPEKRPKSSREGSGGQESSRDKRPL 180  
 DB 121 PATTARGGPKAGSRGRFAGHSAGGSGDRRRAGPEKRPKSSREGSGGQESSRDKRPL 180  
 QY 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQEPHDVAPNGPSAGGLAIP 240  
 DB 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQEPHDVAPNGPSAGGLAIP 240  
 QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGPRSPQREPORVS 300  
 DB 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGPRSPQREPORVS 300  
 QY 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSRGKLVAVKMDLRKQORR 360  
 DB 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSRGKLVAVKMDLRKQORR 360  
 QY 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGALTIDIVTHRMNEEQIAAV 420  
 DB 361 ELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFLEGALTIDIVTHRMNEEQIAAV 420  
 QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTTPY 480  
 DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSILVGTTPY 480  
 QY 481 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNEPPLKAMKIMIRNDLPPRLKNLHK 540  
 DB 481 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNEPPLKAMKIMIRNDLPPRLKNLHK 540  
 QY 541 VPSLKGFLDRLVDRPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
 DB 541 VPSLKGFLDRLVDRPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 7  
 ADC37305  
 ID ADC37305 standard; protein; 438 AA.  
 XX  
 AC ADC37305;  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 138.  
 XX  
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;

cancer; infectious disease; bone disease; AIDS;  
 neurodegenerative disease; ischaemic disorder; Antiinflammatory;  
 immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;  
 Neuroprotective; Nootropic; Cardiant; Gene therapy; human.  
 Homo sapiens.  
 WO2003048202-A2.  
 12-JUN-2003.  
 03-DEC-2002; 2002WO-JP012644.  
 03-DEC-2001; 2001JP-00368692.  
 05-DEC-2001; 2001US-0335829P.  
 03-OCT-2002; 2002JP-00291302.  
 04-OCT-2002; 2002US-0415769P.  
 (ASAH ) ASahi KASEI KK.  
 Matsuda A, Muramatsu S;  
 WPI; 2003-505282/47.  
 N-PSDB; ADC37304.  
 New purified protein that activates nuclear kappa B (NF-kappaB),  
 useful for treating inflammation, autoimmune diseases, cancers,  
 infectious diseases, bone diseases, AIDS, neurodegenerative diseases or  
 ischemic disorders.  
 Claim 1; SEQ ID NO 138; 938pp; English.  
 The present invention relates to novel proteins and their coding  
 sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-  
 kappaB). The proteins and their coding sequences are useful for treating  
 a disease associated with NF-kappaB activation, such as inflammation,  
 autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,  
 neurodegenerative diseases, or ischaemic disorders.  
 Sequence 438 AA;  
 Query Match 71.3%; Score 2202.5; DB 7; Length 438;  
 Best Local Similarity 74.1%; Pred. No. 6.5e-152;  
 Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;  
 1 MFGKRRKVEISAPSNFHRVHTGFDQHQKFTGLPRQWSLIESARRPKPLVDPACT 60  
 1 MFGKRRKVEISAPSNFHRVHTGFDQHQKFTGLPRQWSLIESARRPKPLVDPACT 60  
 61 SIQPGAPKTVIRGSKGAKGALTLILDEFENMSVTRSNLSLRDSDPPPPARARQNGMPEE 120  
 61 SIQPGAPK----- 68  
 121 PATTARGGKAGSRGRFAGHSEAGGSGDRRRAGPEKPKSRREGSGPQESSRDKRPL 180  
 69 ----- 68  
 181 SGPDVGTQPGAGLAKAGLAAGRPNTYPRADTDHPSRGAQGBDVAHPNGSPAGGLAIP 240  
 69 -----GEPHDVAPNGSPAGGLAIP 87  
 241 QSSSSSRPPTTRAGAPSPGVLGPHASEPQLAPPACTPAAPVPGPPGPRSPQREPVYS 300  
 88 QSSSSSRPPTTRAGAPSPGVLGPHASEPQLAPPACTPAAPVPGPPGPRSPQREPVYS 147  
 301 HQFRAALQVNDPCGPRSVLDNFYKIGEGSTGIVCIATVRSSGKLAVKMDLRKQOR 360  
 148 HQFRAALQVNDPCGPRSVLDNFYKIGEGSTGIVCIATVRSSGKLAVKMDLRKQOR 207  
 361 ELLFNEVWIMRDYQHENVVEMVNSYLVGDELWVMEFLGGLTDTVTHTRNNEEQIAAV 420  
 208 ELLFNEVWIMRDYQHENVVEMVNSYLVGDELWVMEFLGGLTDTVTHTRNNEEQIAAV 267

QY 421 CLAVLQALSVLHAQGVIIHRDIKSDSILLTHDGRVKLSDFGFCQAQSVKEVPRKSLVGTPT 480  
 Db 268 CLAVLQALSVLHAQGVIIHRDIKSDSILLTHDGRVKLSDFGFCQAQSVKEVPRKSLVGTPT 327  
 QY 481 WMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPPEPPFLKAMKQIRDLNLPRLKHLK 540  
 Db 328 WMAPELISRLPYGPEVDIWSLIGIMVEMVDGEPPEPPFLKAMKQIRDLNLPRLKHLK 387  
 QY 541 VPSLKGFLDRLVDRDPAQRATAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
 Db 388 VPSLKGFLDRLVDRDPAQRATAELLKHPFLAKAGPPASIVPLMRQNRTR 438  
 RESULT 8  
 AAY55941  
 ID AAY55941 standard; protein; 398 AA.  
 XX AC AAY55941;  
 XX DT 18-FEB-2000 (first entry)  
 XX DE Human PAK5 protein.  
 XX KW Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;  
 KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;  
 KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;  
 KW vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;  
 KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;  
 KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;  
 KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
 KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
 KW myocardial infarction; cardiovascular disease; stroke; renal failure;  
 KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
 KW mesangial disorder; growth regulation; wound healing; T cell activation;  
 KW immunosuppressant.  
 XX OS Homo sapiens.  
 XX PN WO9953036-A2.  
 XX PD 21-OCT-1999.  
 XX PF 13-APR-1999; 99WO-US008150.  
 XX PR 14-APR-1998; 98US-0081784P.  
 XX PA (SUGEN-) SUGEN INC.  
 XX PI Plowman G, Martinez R, Whyte D;  
 XX WPI: 1999-611301/52.  
 XX N-PSDB; AA240493.  
 XX Novel kinase-related polypeptides used for the diagnosis and treatment of  
 XX kinase-related diseases and disorders.  
 XX Disclosure; Page 310-312; 387pp; English.  
 CC This sequence represents a novel STE20-related protein kinase. The  
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide  
 CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,  
 CC ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to  
 CC identify agonists and antagonists, and to raise antibodies. The  
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,  
 CC polypeptides, antibodies, antagonists and agonists may be used to treat  
 CC diseases such as immune-related disorders and diseases (e.g. rheumatoid  
 CC arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.  
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,  
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory  
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial  
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative



CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral  
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,  
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes  
CC mellitus, fibrotic and mesangial disorders. The proteins may also be  
CC useful for cell growth regulation (e.g. in wound healing), T cell  
CC activation, mitosis control, and as immunosuppressants  
XX  
SQ Sequence 398 AA;  
  
Query Match 67.1%; Score 2073; DB 2; Length 398;  
Best Local Similarity 100.0%; Pred. No. 1.5e-142;  
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 194 ASGAKLAAGRPFTNYPRADTDHPSRGAQGEHPHDVAPNGSPAGGLAIPQSSSSSRPPTRA 253  
Db 1 ASGAKLAAGRPFTNYPRADTDHPSRGAQGEHPHDVAPNGSPAGGLAIPQSSSSSRPPTRA 60  
  
QY 254 RGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQEPQVSHQFRAALQLVVD 313  
Db 61 RGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQEPQVSHQFRAALQLVVD 120  
  
QY 314 PGDPRSLDNFIKIGSGTIVCIATVRSCKLVAVKMDLRKQORRELLFNEVIMRDY 373  
Db 121 PGDPRSLDNFIKIGSGTIVCIATVRSCKLVAVKMDLRKQORRELLFNEVIMRDY 180  
  
QY 374 QHENVVEMVNSYLVGDELWVMEFLGEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 433  
Db 181 QHENVVEMVNSYLVGDELWVMEFLGEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 240  
  
QY 434 QGVHRIKDSILLTHDGRVKLSDFGCAQVSKVPRPKSLVGTVPWMAPELISRLPYG 493  
Db 241 QGVHRIKDSILLTHDGRVKLSDFGCAQVSKVPRPKSLVGTVPWMAPELISRLPYG 300  
  
QY 494 PEVDIWSLGMTVEMVDGEPPEYNEPPLKAMKMIRONLPPRLKNLKVSPSLKGFLLRL 553  
Db 301 PEVDIWSLGMTVEMVDGEPPEYNEPPLKAMKMIRONLPPRLKNLKVSPSLKGFLLRL 360  
  
QY 554 VRDPAQRATAAELLKHFFLAKAGPPASIVPLMRQNRTR 591  
Db 361 VRDPAQRATAAELLKHFFLAKAGPPASIVPLMRQNRTR 398  
  
RESULT 9  
AAM38963  
ID AAM38963 standard; protein; 719 AA.  
XX  
AC AAM38963;  
XX  
DT 22-OCT-2001 (first entry)  
DE Human polypeptide SEQ ID NO 2108.  
XX  
KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang JT, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR N-PSDB; AAI58119.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 3; SEQ ID NO 2108; 10078pp; English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 719 AA;  
  
Query Match 56.1%; Score 1734; DB 4; Length 719;  
Best Local Similarity 52.7%; Pred. No. 1.5e-117;  
Matches 385; Conservative 64; Mismatches 126; Indels 156; Gaps 17;  
  
QY 1 MFGKRKRVEISAPSNFHRVHTGPDHOKFTGLPRQWOSLIESARRPKLVDPACIT 60  
Db 1 MFGKKKKKIEISGPNFHRVHTGPDHOKFTGLPRQWOSLIESARRPKLVDPACIT 60  
  
QY 61 STQPGAPKTVRGSKCAKDGALTLLDDEFENSVTSNSLRDSDPPPARA-----R 112  
Db 61 STQPGAPKTVRGSKCAKDGALTLLDDEFENSVTSNSLRDSDPPPARA-----R 120  
  
QY 113 QENGM-----PEEPATTA-----RGG-----PGKA 132  
Db 121 BEENGFTFSQYSSSDTTADYTKYREKSLYGDGDDLDPPYRGSHAAKQNGHVMKMGHEA 180  
  
QY 133 -----GSRGRFAGH-----SEAG 145  
Db 181 YYSEVKPLKSDFAFSAHYSHLSDLSKPSSEYDLKWEYGRASSSPFLDYSFQFTPSRTA 240  
  
QY 146 GSGGDRRA-----GP-----EKRPKSRREGSGGQESSRDKPLSGPDVGTQPAG 192  
Db 241 GTSCKESLAVSESEWSPGLDDYDRRRKSSYLNOTSPQTMR-QRSRSGSLQEPMMSF 299  
  
QY 193 LASGAKL-AAGRPFTNY-----PRADTDH-----PSRGAQGEHPHDVAPNGP 232  
Db 300 GASAFKTHPQGHNSYNTYPRLSSEPTMCIPKVDYDRAQMVLPSPLSGS-----DTPYRGP 354  
  
QY 233 SAGGLAIPOS-----SSSSSRPPTRAGAPSPGVLGPHASEPQLAPPACTP----- 278  
Db 355 A-----KLQSQKSGYSSSSSHQVPSGYHKA-----TLYHPSLQSSSQYSTASLSSLSL 406  
  
QY 279 AAPAVPGPGPRSPQEPQVSHQFRAALQLVVDGPDPRSYLDFIKIGSGTIVCIAT 338  
Db 407 SSSSTYPPPSGSSSDQQPSRVSHEQFRAALQLVVDGPDPRSYLDFIKIGSGTIVCIAT 466  
  
QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFL 398

Db	467	TEKHTGQVAVKMDLRKQQRRELLFNEWIMRDYHHDNVDMYNSLVGDGLWVMEFL	526
Qy	399	EGGALTDIVTRMNEEQIAAACLAVLAQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSD	458
Db	527	EGGALTDIVTRMNEEQIATVCLSVLRALSVLHNQGVHHRDIKSDSILLTSDGRIKUSD	586
Qy	459	FGPCQVSKVEPRKSLVGTGYWMAPELISRLPYGPEVDIWSLGIWVIMVDGEPYPFNE	518
Db	587	FGCAQVSKVEPRKSLVGTGYWMAPEVLSRLPYGTEVDIWSLGIWVIMIDGEPYPFNE	646
Qy	519	PPLKAMKIRDNLPRLKXNLHKVSPSLKGFDRLLVRDPAQRATAAELLKHFPFLAKAGPP	578
Db	647	PPLQAMRRIRDSLPFRVLDLHKVSVLVRGFLDMLVLRPESQRTATQELLCHFPFLKLAGPP	706
Qy	579	ASIVPLMFQNR	589
Db	707	SCIVPLMFQNR	717
RESULT 10			
AAB65705			
ID	AAB65705 standard; protein; 719 AA.		
XX			
AC	AAB65705;		
DT	27-MAR-2001 (first entry)		
XX			
DE	Novel protein kinase, SEQ ID NO: 234.		
XX			
KW	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;		
KW	immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;		
KW	dermatological; antidiabetic; antifertility; gene therapy; vaccine;		
KW	immune disorder; cardiovascular disease; neurodegenerative disease;		
KW	cancer; autoimmune disorder; stroke; inflammatory bowel disease;		
KW	inflammatory pelvic disease; multiple sclerosis; psoriasis.		
OS	Homo sapiens.		
XX			
PN	WO200073469-A2.		
XX			
FD	07-DEC-2000.		
XX			
PF	26-MAY-2000; 2000WO-US014842.		
XX			
PR	28-MAY-1999; 99US-0136503P.		
XX			
PA	(SUGE-) SUGEN INC.		
XX			
PI	Plowman GD, Martinez R, Whyte D, Sudersanam S;		
XX			
DR	WPI; 2001-032161/04.		
DR	N-PSDB; AAF44734.		
XX			
PT	Nucleic acids encoding kinase polypeptides, useful for diagnosing and		
PT	treating immune-related diseases and disorders, cardiovascular disease,		
PT	neurodegenerative diseases and/or cancers.		
XX			
PS	Claim 10; Fig 1; 310pp; English.		

CC	stress related disorders, chronic inflammatory bowel disease, chronic
CC	inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC	psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC	disorders
XX	
SQ	Sequence 719 AA;
	Query Match      56.0%; Score 1731; DB 4; Length 719;
	Best Local Similarity 52.4%; Pred. No. 2.6e-117;
	Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17
QY	1 MFGRKKRKEVLSAPSNFHRVHTGFDQEQKFTGLPROMWQSILIESARRPKPLVDPACTI 60
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	1 MFGRKKKRIELSGSFNFRVHTGFDPOEQKFTGLPQOWHSLLATANRPKWDPSCIT 60
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	61 SIQPGAKPTIVRGSKAGDXGADLTLLDLDFENMSVTRNSLRDSSPPPPARA-----R 112
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	61 PIQLPMKTIVRGNKPCKETSINGLLEDFNISVTRNSLRKESPTPDQGASSHPGHA 120
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	113 QENGK-----PEEPATTA-----GG-----PGKA 132
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	121 EENGFIITSQYSSESDTTADVTTKYREKSLYGDDLDPYIRGSHAAKONGHVMMKHGHEA 180
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	133 -----GSRGPFAGH-----PRADTDH-----PSRGAQGEHDVAQNGP 145
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	181 YYSEVKPLKSFARFSAHYSHLDLSLKPEYSVDLKWEYQRASSSPLDYSPQFTPSRTA 240
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	146 GSGDRRA-----GP-----EKRPKSREGSGGPOEQRSDRKRPISGPDVGTP-QPA 191
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	241 GTSGCSKESLAYSESWGPSDDYDRRKSSYLNOTSPQTWMR-QRSRSGSLOBPMPMF 299
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	192 GLASCAKLAAGRPNTY-----PRADTDH-----PSRGAQGEHDVAQNGP 232
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	300 GASAFKTHPOGHSYNSYTYPLBSBETMCIPKVVDYDRAQMVLSPPLSGS-----DTVPGRP 354
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	233 SAGGLAIPOS-----SSSSSRPPTRARCAPSPGVLGPHASEPQLAPPACTP----- 278
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	355 A----KLPQSQSKSGYSSSSHQPSGYHKA---TLXHHPSLQSSQXIYSTASYLSLSL 406
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	279 AAPAVGPPGPRSPQREPQRVSHQFPRAALQIUVDPGDPPRSVDNFNKIGEGSTGIVCITA 338
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	407 SSSTYPSPSGSSSDQQPSRYSHQFPRAALQIUVSPGDPREYLANFIKIGESTGIVCITA 466
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	339 TVRSSGKLAVAKMDLRKQQRRELLFNFWIMRDYOHENVYMNSYLVGDDELVVWVEFL 398
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	467 TEKTKGQVAVKMDLRKQQRRELLFNFWIMRDVHHNVVDVMYSYLVGDDELVVWVEFL 526
DB	:::     :::     :::     :::     :::     ~::~   :::     :::
QY	399 EGGALTDTVTRMNEEQIAAVCLAVLOALSVLHAQGVITHRIDIKSDSIILLTHDGRVKUSD 458
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	527 EGGALTDTVTRMNEEQIATVCLSVLRALSVLHHNQGVITHRIDIKSDSIILLTSDGRIKLSD 586
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	459 GFCAQVSKEVPRRKSLVGTPIYWMAPELISRLPYCPDVDIWSLGMTWIEMWDGEPPIYNE 518
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	587 GFCAQVSKEVPRRKSLVGTPIYWMAPEVISRLPYGTEVDIWSLGMTWIEMWDGEPPIYNE 646
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	519 PPLKAMKMIRONLPPRLKNLHKVSPSLKGFDRLILVRDPAQKATAELLKHFPLAKAGPP 578
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	647 PPLQAMRRIRUSLIPPRVKDLHKVSVLRGFLDMLVRFSPQKATAEQLLGHFPLKLAGPP 706
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	579 ASIVPLMRQNR 589
DB	:::     :::     :::     :::     :::     :::     :::     :::
QY	707 SCIVPLMRQYR 717
DB	:::     :::     :::     :::     :::     :::     :::     :::



PT New nucleic acid encoding p21-activated kinase 5 protein for inducing an  
PT immune response, treating cancers, angiogenesis-related disorders,  
PT disorders of the central nervous system and immune-related disorders.  
XX  
XX Claim 28; Page 33; 76pp; English.  
XX  
CC The present sequence is human p21-activated kinase 5 (PAK5) which is a  
CC serine-threonine kinase. PAK5 is useful for inducing an immune response  
CC in a mammal against PAK5 polypeptide. PAK5 proteins are useful in  
CC regulating cell proliferation, cell migration, cell differentiation, and  
CC cytoskeletal organisation, gene expression, cell cycle progression, and  
CC cell death. PAK5, is useful in the search for novel agents that can  
CC modify and/or control the above processes. PAK5 DNA is useful for  
CC screening restriction fragment length polymorphism (RFLP) associated with  
CC certain disorders, as well as for genetic mapping. PAK5 DNA is also  
CC useful as diagnostic tools for probing gene expression in various  
CC tissues. PAK5 polypeptides are also useful as antigens for raising  
CC antibodies, and for screening compounds that modulate the activity of  
CC PAK5. PAK5 is also useful in pharmaceutical compositions, and in the  
CC manufacture of medicaments for treating diseases such as cancers,  
CC angiogenesis-related disease, diseases of the central nervous system and  
CC diseases due to inappropriate activation of immune responses. PAK5 DNA is  
CC also useful in gene therapy  
XX  
XX Sequence 719 AA;

Query Match 56.0%; Score 1730; DB 4; Length 719;  
Best Local Similarity 52.4%; Pred. No. 3e-117;  
Matches 383; Conservative 65; Mismatches 127; Indels 156; Gaps 17;  
QY 1 MFGKKKRVISAPNFEHRVHTGPDQHQKFTGLPQWQSILIBESARRPKPLVDPACT 60  
DB 1 MFGKKKKKIEISGPSNFEHRVHTGPDQHQKFTGLPQWQSILIBESARRPKPLVDPACT 60  
QY 61 STOPGAPKTIVRGSGAKDGLTLLDEPNNSVTRNSLRDSDPPPARA-----R 112  
DB 61 PQLAPMKTIVRGSGAKDGLTLLDEPNNSVTRNSLRDSDPPPARA-----R 112  
QY 113 QENGM-----PEEPATTA-----RGG-----PGKA 132  
DB 121 EENGPIFISQYSESDTADYTEKYREKSLYGDLDLPYRSGHAAKQNHVMKMGHA 180  
QY 133 -----GSRGRFAGH-----SEAG 145  
DB 181 YXSEVKPLKSDFAFSAHYSHLDSLKPSEYSLKWEYQRASSPLDYSFQTPSRTA 240  
QY 146 GSGDERRA-----GP-----EKRPKSGREGSGPQESSRDXPLSGPDVGTGTP-QPA 191  
DB 241 GTSGGCKSLAYSESEWGPGLDDYDRRPKSSYLNTSPQPTWR-QRSRSGSLQBPMPFF 299  
QY 192 GLASGAKLAAGRPFTNY-----PRADTDH-----PSRGAQGEHDVAPNGP 232  
DB 300 GASAFKTHPQHSYNSYTPRLSEPTMCIPKVDYDRAQVMSLPPLSGS-----DTPRGP 354  
QY 233 SAGGLAIPOS-----SSSSSRPPTARGAPSGVLGPHASEPQLAPPACTP----- 278  
DB 355 A-----KLPOQSKSGSYSSSHOVPSGYHKA-----TLYHPSLQSSQYISTASYLSLSL 406  
QY 279 AAPAVGPGPSPQEPORVSHQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIA 338  
DB 407 SSSYTPPPSWGSSGSDQSRVSHQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIG 466  
QY 339 TVRSSGKLVAVKMDLRKQKRELLFNEVVIIRDYOHENNVEMYSYLVGDELWVMEFL 398  
DB 467 TEKHTGQVAVKMDLRKQKRELLFNEVVIIRDYOHENNVEMYSYLVGDELWVMEFL 526  
QY 399 EGALTDIIVTHRMNEEQIAVCLAVLQALSVLHQAQVTHRDIKSDSILLTHDGRVKLSD 458  
DB 527 EGALTDIIVTHRMNEEQIATVCLSVLRAVSLHQAQVTHRDIKSDSILLTHDGRVKLSD 586  
QY 459 FGCAQVSKEVPRKSLVGTGPFYMAPELISRLPYGPEVDIWSLGIWVIMVDPGEPPYFNE 518  
DB 587 FGCAQVSKEVPRKSLVGTGPFYMAPELISRLPYGPEVDIWSLGIWVIMVDPGEPPYFNE 646

QY 519 PPLKAMKIMRDNLPRLLKHLKVSPLKGLFDRLLVRDPAQRATAELLKHPFLAKAGPP 578  
DB 647 PPLQAMRIRDSLPVRVLDLHKVSSVLGFLDMLVREPSQRATAELLGHPFLAKAGPP 706  
QY 579 ASIVPLMQRNR 589  
DB 707 SCIVPLMQRNR 717  
XX  
XX ADEI5851  
XX ADEI5851 standard; protein; 293 AA.  
XX ADEI5851;  
XX 29-JAN-2004 (first entry)  
XX PAK4KD protein.  
XX PAK4KD protein.  
XX Homo sapiens.  
XX WO2003087816-A1.  
XX 23-OCT-2003.  
XX 08-APR-2003; 2003WO-US010878.  
XX 09-APR-2002; 2002US-0371018P.  
XX 02-DEC-2002; 2002US-0430567P.  
XX (STRU-) STRUCTURAL GENOMIX INC.  
XX  
XX Anthonyamy SS, Feil I, Buchanan SG, Post KW, Liu Y, Lorber D;  
XX WPI; 2003-853974/79.  
XX  
XX Producing a computer-readable database comprising the three-dimensional  
XX molecular structural coordinates of a binding pocket of a PAK4KD protein,  
XX comprises introducing the structural coordinates into a computer.  
XX  
XX Claim 17; SEQ ID NO 5; 421pp; English.  
XX  
XX The present invention relates to producing a computer-readable database  
XX comprising the three-dimensional molecular structural coordinates of a  
XX binding pocket of a PAK4KD protein, comprising introducing the structural  
XX coordinates into a computer to produce a database containing the  
XX molecular structural coordinates of the protein or binding pocket. The  
XX method is useful for producing a machine-readable database for  
XX identifying and designing inhibitors, activators and mutants of PAK4KD,  
XX PAK4KD crystals and compounds or compositions that affect PAK4KD  
XX activity. The present sequence represents a primer of the invention.  
XX  
XX Sequence 293 AA;

Query Match 48.6%; Score 1502; DB 7; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.9e-101;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 300 SHEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQOR 359  
DB 2 SHEQFRAALQLVDPDPRSYLDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQOR 61  
QY 360 RELLENNVIMRDYOHENNVEMYSYLVGDELWVMEFLGEGALTDIIVTHRMNEEQIAA 419  
DB 62 RELLENNVIMRDYOHENNVEMYSYLVGDELWVMEFLGEGALTDIIVTHRMNEEQIAA 121  
QY 420 VCLAVLQALSVLHQAQVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRKSLVGTGP 479  
DB 122 VCLAVLQALSVLHQAQVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRKSLVGTGP 181





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:58:42 ; Search time 40.8485 Seconds  
(without alignments)  
746.929 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGKKRKRVEISAPNSFEHR.....LAKAGPPASIVPLMRQNR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pdp.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pdp.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pdp.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pdp.\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS COMB.pdp.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3090	100.0	591	3	US-09-082-737-2
2	3090	100.0	591	4	US-09-688-188B-103
3	3090	100.0	591	4	US-09-718-032-2
4	3090	100.0	591	4	US-09-291-417D-103
5	2073	67.1	398	4	US-09-688-188B-30
6	2073	67.1	398	4	US-09-291-417D-30
7	1473.5	47.7	681	4	US-09-688-188B-29
8	1473.5	47.7	681	4	US-09-291-417D-29
9	1470.5	47.6	681	4	US-09-765-815-2
10	1277	41.3	250	3	US-09-082-737-3
11	1277	41.3	250	4	US-09-718-032-3
12	912	29.5	544	2	US-08-935-760-2
13	907	29.4	544	4	US-09-688-188B-95
14	907	29.4	544	4	US-09-291-417D-95
15	900	29.1	524	2	US-08-615-942A-2
16	900	29.1	524	4	US-09-237-325-2
17	899	29.1	544	3	US-08-559-397A-19
18	894	28.9	506	1	US-08-369-780-2
19	894	28.9	506	1	US-08-475-682-2
20	894	28.9	506	1	US-08-780-833-2
21	894	28.9	506	1	US-08-636-036-2
22	894	28.9	506	3	US-09-918-509-2
23	894	28.9	506	3	US-09-108-262-2
24	894	28.9	506	4	US-09-688-188B-94
25	894	28.9	506	4	US-09-291-417D-94
26	891.5	28.9	545	2	US-08-935-760-4
27	891.5	28.9	545	4	US-09-688-188B-93

28	891.5	28.9	545	4	US-09-291-417D-93	Sequence 93, Appl
29	867	28.1	544	3	US-08-559-397A-29	Sequence 29, Appl
30	849	27.5	544	3	US-08-559-397A-30	Sequence 30, Appl
31	833.5	27.0	465	2	US-08-114-555A-2	Sequence 2, Appl
32	821	26.6	694	3	US-08-559-397A-31	Sequence 31, Appl
33	814.5	26.4	465	3	US-08-559-397A-2	Sequence 2, Appl
34	804	26.0	305	4	US-09-765-815-10	Sequence 10, Appl
35	782	25.3	793	3	US-09-588-256-10	Sequence 10, Appl
36	769	24.9	268	2	US-08-852-743-3	Sequence 3, Appl
37	769	24.9	268	3	US-09-185-370-3	Sequence 3, Appl
38	741	24.0	250	4	US-09-718-032-4	Sequence 4, Appl
39	719.5	23.3	244	4	US-09-163-507-1	Sequence 1, Appl
40	717.5	23.2	271	2	US-08-852-743-4	Sequence 4, Appl
41	717.5	23.2	271	3	US-09-185-370-4	Sequence 4, Appl
42	712	23.0	245	4	US-09-163-507-3	Sequence 3, Appl
43	706	22.8	244	4	US-09-163-507-2	Sequence 2, Appl
44	704	22.8	251	3	US-09-082-737-5	Sequence 5, Appl
45	699	22.6	250	4	US-09-718-032-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-082-737-2  
; Sequence 2, Application US/09082737  
; Patent No. 6013500  
; GENERAL INFORMATION:  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/  
; TITLE OF INVENTION: Threonine Kinase  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11230  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/082,737  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/55311  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 591 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-082-737-2

Query Match 100.0%; Score 3090; DB 3; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.3e-191;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGKKRKRVEISAPNSFEHRVHTGDFDQHEQKFTGLPRQWQSLEESARRPKPLVDPACIT 60  
Db 1 MFGKKRKRVEISAPNSFEHRVHTGDFDQHEQKFTGLPRQWQSLEESARRPKPLVDPACIT 60  
QY 61 STQPGAPKTVRGSGAKDGKALTLLDFFNNSVTRNSLRDSSPPPPARAPQENGMBEE 120



Db 61 SIQCAPKTIVRGSKAGKDGALITLLDDEFNMVSTRNSLRDSDPPPARAQENGMPEE 120  
QY 121 PATTARGGPKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRL 180  
Db 121 PATTARGGPKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRL 180  
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Db 241 QSSSSSSRPPTTRARGAPSGVLGHASEPQLAPPACTPAAPVPPGPPGPPSPQRPQVRS 300  
QY 301 HQFRAALQLVDPGDRSYLDNFIKIGEGSTGIICATVRSSGKLVAVKMDLRKQRR 360  
Db 301 HQFRAALQLVDPGDRSYLDNFIKIGEGSTGIICATVRSSGKLVAVKMDLRKQRR 360  
QY 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAV 420  
Db 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAV 420  
QY 421 CLAVLQALSVLHAQGVTHIRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTPY 480  
Db 421 CLAVLQALSVLHAQGVTHIRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTPY 480  
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKIMIRNDLPPRLKNLHK 540  
Db 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKIMIRNDLPPRLKNLHK 540  
QY 541 VSPSLKGFLLDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
Db 541 VSPSLKGFLLDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

## RESULT 2

US-09-688-188B-103  
; Sequence 103, Application US/09688188B  
; Patent No. 6656716  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0328  
; CURRENT FILING DATE: US/09/688,188B  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 09/291,417  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 103  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-688-188B-103

Query Match 100.0%; Score 3090; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.3e-191;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MFGRKKRVEISAPSNFHRVHTGFDQHEOKFTGLPRQWOSLIEESARRPKPLVDPAKIT 60  
QY 61 SIQCAPKTIVRGSKAGKDGALITLLDDEFNMVSTRNSLRDSDPPPARAQENGMPEE 120  
Db 61 SIQCAPKTIVRGSKAGKDGALITLLDDEFNMVSTRNSLRDSDPPPARAQENGMPEE 120  
QY 121 PATTARGGPKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRL 180  
Db 121 PATTARGGPKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRL 180

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QY 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240  
Db 181 SGPDVGTTPQAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEHVDVAPNGPSAGGLAIP 240  
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Db 241 QSSSSSSRPPTTRARGAPSGVLGHASEPQLAPPACTPAAPVPPGPPGPPSPQRPQVRS 300  
QY 301 HQFRAALQLVDPGDRSYLDNFIKIGEGSTGIICATVRSSGKLVAVKMDLRKQRR 360  
Db 301 HQFRAALQLVDPGDRSYLDNFIKIGEGSTGIICATVRSSGKLVAVKMDLRKQRR 360  
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Db 361 ELLFNEVIMRDYQHENVVEMVNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEEQIAAV 420  
QY 421 CLAVLQALSVLHAQGVTHIRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTPY 480  
Db 421 CLAVLQALSVLHAQGVTHIRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSILVGTPY 480  
QY 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKIMIRNDLPPRLKNLHK 540  
Db 481 WNAPELISRLPYGPEVDIWSLGIWVEMVDPGPPYFNEPPLKAMKIMIRNDLPPRLKNLHK 540  
QY 541 VSPSLKGFLLDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591  
Db 541 VSPSLKGFLLDRLLVRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

## RESULT 3

US-09-718-032-2  
; Sequence 2, Application US/09718032  
; Patent No. 6657168  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE  
; FILE REFERENCE: 575/55311-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/718,032  
; CURRENT FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: PCT/US99/11341  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 09/082,737  
; PRIOR FILING DATE: 1998-05-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 2  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: human  
US-09-718-032-2

Query Match 100.0%; Score 3090; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.3e-191;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGRKKRVEISAPSNFHRVHTGFDQHEOKFTGLPRQWOSLIEESARRPKPLVDPAKIT 60  
Db 1 MFGRKKRVEISAPSNFHRVHTGFDQHEOKFTGLPRQWOSLIEESARRPKPLVDPAKIT 60  
QY 61 SIQCAPKTIVRGSKAGKDGALITLLDDEFNMVSTRNSLRDSDPPPARAQENGMPEE 120  
Db 61 SIQCAPKTIVRGSKAGKDGALITLLDDEFNMVSTRNSLRDSDPPPARAQENGMPEE 120  
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Db 121 PATTARGGPKAGSRGRFAGHSEAGGSGDRRRRAGPEKRPKSSREGSGGPOESSDRKRL 180  
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DB 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
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DB 301 HEQFRAALQLVDPGPRSYLNDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRR 360
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DB 361 ELLFNEVIMRDYQHENVVMYNSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAV 420
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DB 421 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSLSVGTPT 480
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DB 541 VSPSLKGFLLRDLVRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 4
US-09-291-417D-103
; Sequence 103, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-103

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKRVESAPSNEFHRVHTGFDQHQKFTGLPRQWSLIESARRPKPLVDPACT 60
DB 1 MFGKRRKRVESAPSNEFHRVHTGFDQHQKFTGLPRQWSLIESARRPKPLVDPACT 60
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QY 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIP 240
DB 181 SGPDVCTPQAGLASAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
DB 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVS 300
QY 301 HEQFRAALQLVDPGPRSYLNDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRR 360
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DB 301 HEQFRAALQLVDPGPRSYLNDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRR 360
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DB 361 ELLFNEVIMRDYQHENVVMYNSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAV 420
QY 421 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSLSVGTPT 480
DB 421 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSLSVGTPT 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYPYFNEPPLKAMKMIKMDLPPRLKMLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYPYFNEPPLKAMKMIKMDLPPRLKMLHK 540
QY 541 VSPSLKGFLLRDLVRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 541 VSPSLKGFLLRDLVRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 5
US-09-688-188B-30
; Sequence 30, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-30

Query Match 67.1%; Score 2073; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.3e-126;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIPQSSSSSRPPTRA 253
DB 1 ASGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPSAGGLAIPQSSSSSRPPTRA 253
QY 254 RGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVSHEQFRAALQLVVD 313
DB 61 RGAPSPGVLGPHASEPOLAPPACTPAAPAVPGPPGPRSPQREPORVSHEQFRAALQLVVD 120
QY 314 PGDPRSGLDNFNIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRRLLFNEVIMRDY 373
DB 121 PGDPRSGLDNFNIKIGEGSTGIVCIATVRSRSGKLVAVKMDLRKQRRLLFNEVIMRDY 180
QY 374 QHENVVMYNSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 433
DB 181 QHENVVMYNSYLVGDELWVMEFLEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 240
QY 434 QGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSLSVGTPTWMAPELISRLPYG 493
DB 241 QGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSLSVGTPTWMAPELISRLPYG 300
QY 494 PEVDIWSLGIWMIEMVDGEPYPYFNEPPLKAMKMIKMDLPPRLKMLHKVPSLKGFLDRLL 553
DB 301 PEVDIWSLGIWMIEMVDGEPYPYFNEPPLKAMKMIKMDLPPRLKMLHKVPSLKGFLDRLL 360
QY 554 VRDPAQRTAAELLKHPFLAKAGPPASIVPLMRQNRTR 591
```

Db 361 VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNR 398  
|||||

RESULT 6  
US-09-291-417D-30  
; Sequence 30, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329  
; CURRENT APPLICATION NUMBER: US/09/291,417D  
; CURRENT FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 1999-04-13  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 398  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-291-417D-30

Query Match 67.1%; Score 2073; DB 4; Length 398;  
Best Local Similarity 100.0%; Pred. No. 4.3e-126; Mismatches 0; Indels 0; Gaps 0;  
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 194 ASGAKLAAGRPNTYPRADTDHPSGAQGEHDVAPNGPSAGGLAIPQSSSSSRPPTRA 253  
Db 1 ASGAKLAAGRPNTYPRADTDHPSGAQGEHDVAPNGPSAGGLAIPQSSSSSRPPTRA 60  
QY 254 RGAPSGVLGPHASEPOLAPPACTPAAPVPGPGPSQRPQVSHQFPAALQLVVD 313  
Db 61 RGAPSGVLGPHASEPOLAPPACTPAAPVPGPGPSQRPQVSHQFPAALQLVVD 120  
QY 314 PGDPRSYLNFNFKIGEGSTGIVCIATVRSSGKLVAKKMDLRKQRRLLFNEVIMRDY 373  
Db 121 PGDPRSYLNFNFKIGEGSTGIVCIATVRSSGKLVAKKMDLRKQRRLLFNEVIMRDY 180  
QY 374 QHENVVYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEBQIAAVCLAVLQALSVLHA 433  
Db 181 QHENVVYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEBQIAAVCLAVLQALSVLHA 240  
QY 434 QGVHRIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSIVGTPTWMAPELISRLPYG 493  
Db 241 QGVHRIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSIVGTPTWMAPELISRLPYG 300  
QY 494 PEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMIKMDLRKQRRLLFNEVIMRDY 553  
Db 301 PEVDIWSLGIWVEMVDGPPYFNEPPLKAMKMIKMDLRKQRRLLFNEVIMRDY 360  
QY 554 VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNR 591  
Db 361 VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNR 398  
|||||

RESULT 7  
US-09-688-188B-29  
; Sequence 29, Application US/09688188B  
; Patent No. 6656716  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0328  
; CURRENT APPLICATION NUMBER: US/09/688,188B  
; CURRENT FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 09/291,417  
; PRIOR FILING DATE: 1999-04-14

; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 681  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-688-188B-29

Query Match 47.7%; Score 1473.5; DB 4; Length 681;  
Best Local Similarity 48.1%; Pred. No. 3.1e-87;  
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;  
QY 4 KKKRVEISAPSNPEHRVHTGFDQHEOKFTGLPROMQSLIEESARRPKPLVDPAITSIQ 63  
Db 5 KKKRPEISAFONFOHRVHTSFDPKGEKFGVGLPPQWQNL-DTLRRPEVVDPSRITRVQ 63  
QY 64 PGAPKTIIVRGSGKAGDGAATLLDEFENNSVTRNSLRDSDPPPARAR----- 112  
Db 64 LQPMKTVVRGSAAMPVDGYISGLNDIQKLSVISSNTLRGSRPTSRRAQSLGLLGDHWA 123  
QY 113 -----QENG-----PEPATTARGCPKAGSRG--- 136  
Db 124 TDPDMYLOSPOSERTDPHGLYLSNCGTTPAGHKOMPPEPQSPRVLPNGLAQAQSLGPA 183  
QY 137 RFAGHSEAG---GGSGDRRRAGPEKRRPKSSREGSGGPOESSRDKRPLS-----GP 183  
Db 184 EFQASQRLQIGACIQSPFGASPTGTNRHGMAAKHGSEARFQSCLVGSATGRPG 243  
QY 184 DVTGPPQAGLASGAKLAAGRPNTYPRADTDHPSGAQGEHDVAPNGPSAGGLAIPQS 243  
Db 244 E-GSPSPKTRSSSLKRRFRSM-FLSTAATAPPSSSKPQPPQSKPN----- 288  
QY 244 SSSSP-----TPARGASP---CVLGPASEPOLAPPACTPAAPVPGPGPS 291  
Db 289 -SSFPQKNDPPSLVAKAQLSPSQPVGTFTSPLTTSQKSLRTAPATGQLPGRSS 347  
QY 292 POREPQ-----VSHEQFRAALQLVVDGDPDRSYL 321  
Db 348 PAGESRTWHAQISTSNLYLPQDPTVAKGALAGEDTGVVTHEQFKAALRMVVDGDPRLLL 407  
QY 322 DNFIKIGSGSTGIVCIATVRSSGKLVAKKMDLRKQRRLLFNEVIMRDYOHENVVEM 381  
Db 408 DSYVXIGSGSTGIVCLAREKHSGRQVAVKQMDLRKQRRLLFNEVIMRDYOHENVVEM 467  
QY 382 YNSYLVGDELWVMEFLEGGALTDIVTHTRMNEBQIAAVCLAVLQALSVLHAQGVHRI 441  
Db 468 YKSYLVGDELWVMEFLEGGALTDIVSQVRLNEEQIATVCEAVLQALAYLHAQGVHRI 527  
QY 442 KSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSIVGTPTWMAPELISRLPYGPEVDIWSL 501  
Db 528 KSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSIVGTPTWMAPEVLSRLPYATEVDIWSL 587  
QY 502 GIMVEMVDGPPYFNEPPLKAMKMIKMDLRKQRRLLFNEVIMRDYOHENVVEM 561  
Db 588 GIMVEMVDGPPYFSDSPQAMKRLDSSPPKLNKSHKVSPLVRLDFLERMLVRDQERA 647  
QY 562 TAAELLKHPFLAKAGPPASIVPLMRQNR 589  
Db 648 TAAELLKHPFLKQTLPECLVPLIQYR 675  
|||||

RESULT 8  
US-09-291-417D-29  
; Sequence 29, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329

FILE REFERENCE: 01948/068002  
CURRENT APPLICATION NUMBER: US/09/291,417D  
CURRENT FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 60/081,784  
PRIOR FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 29  
LENGTH: 681  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-291-417D-29

Query Match 47.7%; Score 1473.5; DB 4; Length 681;  
Best Local Similarity 48.1%; Pred. No. 3 le-87;  
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;

QY 4 KKKKRVISAPNFEHRVHTGDFDQHQKFTGLPRMQSLIESARRPKPLVDPACITSIQ 63  
D 5 KKKKRVISAPNFEHRVHTGDFDQHQKFTGLPRMQSLIESARRPKPLVDPACITSIQ 63  
QY 64 PGAPKTIIVRGSKGAKDGLTLLIDFENMVSRTSLRDSPPPPARAR-----112  
D 64 LQPMKTVVRGSAWPDVGYISGLNDIQKLSVSSNTLRGSPTRRRRAQSLGLLGDHWA 123  
QY 113 -----QENGM-----PEEPATTARGGPKGAGSRG--136  
D 124 TDPDMYLOSPQSERDTPHGLYLSGNGGTGAGHKQMPWPEQSPRVLNGLAQAQSLGPA 183  
QY 137 RFAGHSEAG---GGSGDRRRAGEKPKSRREGSGGPGQSSRDKRPLS-----GP 183  
D 184 EFQASQRCQLQACGLQSSPPGASPTGTNRHGMKAAGHSEARQSCLVGSATGRPGG 243  
QY 184 DVGTPQAGLAGAKLAACRPNTYPRADTDPHSCAQGEQPHDVAENGSAAGLAIPQSS 243  
D 244 E-GSPSPKTRSLKRLFRSM-FLSTAATAPSSSKPGPPPOSKPN-----288  
QY 244 SSSSRPP-----TRARGAPSP---GVLGPHASEPQLAPPACTPAAPVPPGPRSS 291  
D 289 -SSFRPPQKNDPSSLVAKAQSLSDDQPVGTFTSPLTSSPQKSLRTAPATQQLPGRSS 347  
QY 292 POREPOR-----VSHEQFRAALQVLVDPGDPSSYL 321  
D 348 PAPSPTWHAQISTNSLYLPQDPTVAKGALAGEDTGVVTHEQFKAALRMVVDQDPRLL 407  
QY 322 DNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYOHENNVEM 381  
D 408 DSYVKIGESTGIVCIAREKHSGRQVAVKMDLRKQORRELLFNEVIMRDYOHENNVEM 467  
QY 382 YNSYLVDGLWVMEFEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVIRHDI 441  
D 468 YKSYLVGEELWLMFELQGGALTDIVSOVRLNEEQIATVCEAVLQALSVLHAQGVIRHDI 527  
QY 442 KSDSILLTHDGRVKLSDFGFCQAVSKEVPRKSLVGTPTWMAPELISRLPYGGEVDIWSL 501  
D 528 KSDSILLTHDGRVKLSDFGFCQAVSKEVPRKSLVGTPTWMAPELISRLPYGGEVDIWSL 587  
QY 502 GIMVIMVDGEPYPFNEPPLKAMKMRDNLPRKLNHVKVSPSLKGLFDRLLVRDPAORA 561  
D 588 GIMVIMVDGEPYPFSDSPVQAMKRLRDSPPPKLNKSHKVSPLRDFLERMLVRDPOERA 647  
QY 562 TAAELKHPPFLAKAGPPASIVPLMRQNR 589  
D 648 TAQELLDHFPFLQTLGPECLVPLIQLYR 675

## RESULT 9

US-09-765-815-2  
Sequence 2, Application US/09765815  
Patent No. 6673586  
GENERAL INFORMATION:  
APPLICANT: Balk, Steven  
TITLE OF INVENTION: No. 6673586el Steroid Hormone Receptor  
TITLE OF INVENTION: Interacting Protein Kinase

## RESULT 10

US-09-082-737-3  
Sequence 3, Application US/09082737  
Patent No. 6013500  
GENERAL INFORMATION:  
APPLICANT: Minden, Audrey  
TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/

FILE REFERENCE: 01948/068002  
CURRENT APPLICATION NUMBER: US/09/765,815  
CURRENT FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 60/176,859  
PRIOR FILING DATE: 2000-01-19  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 681  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-765-815-2

Query Match 47.6%; Score 1470.5; DB 4; Length 681;  
Best Local Similarity 48.0%; Pred. No. 4 le-87;  
Matches 330; Conservative 70; Mismatches 169; Indels 119; Gaps 12;

QY 4 KKKKRVISAPNFEHRVHTGDFDQHQKFTGLPRMQSLIESARRPKPLVDPACITSIQ 63  
D 5 KKKKRVISAPNFEHRVHTGDFDQHQKFTGLPRMQSLIESARRPKPLVDPACITSIQ 63  
QY 64 PGAPKTIIVRGSKGAKDGLTLLIDFENMVSRTSLRDSPPPPARAR-----112  
D 64 LQPMKTVVRGSAWPDVGYISGLNDIQKLSVSSNTLRGSPTRRRRAQSLGLLGDHWA 123  
QY 113 -----QENGM-----PEEPATTARGGPKGAGSRG--136  
D 124 TDPDMYLOSPQSERDTPHGLYLSGNGGTGAGHKQMPWPEQSPRVLNGLAQAQSLGPA 183  
QY 137 RFAGHSEAG---GGSGDRRRAGEKPKSRREGSGGPGQSSRDKRPLS-----GP 183  
D 184 EFQASQRCQLQACGLQSSPPGASPTGTNRHGMKAAGHSEARQSCLVGSATGRPGG 243  
QY 184 DVGTPQAGLAGAKLAACRPNTYPRADTDPHSCAQGEQPHDVAENGSAAGLAIPQSS 243  
D 244 E-GSPSPKTRSLKRLFRSM-FLSTAATAPSSSKPGPPPOSKPN-----288  
QY 244 SSSSRPP-----TRARGAPSP---GVLGPHASEPQLAPPACTPAAPVPPGPRSS 291  
D 289 -SSFRPPQKNDPSSLVAKAQSLSDDQPVGTFTSPLTSSPQKSLRTAPATQQLPGRSS 347  
QY 292 POREPOR-----VSHEQFRAALQVLVDPGDPSSYL 321  
D 348 PAPSPTWHAQISTNSLYLPQDPTVAKGALAGEDTGVVTHEQFKAALRMVVDQDPRLL 407  
QY 322 DNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYOHENNVEM 381  
D 408 DSYVKIGESTGIVCIAREKHSGRQVAVKMDLRKQORRELLFNEVIMRDYOHENNVEM 467  
QY 382 YNSYLVDGLWVMEFEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVIRHDI 441  
D 468 YKSYLVGEELWLMFELQGGALTDIVSOVRLNEEQIATVCEAVLQALSVLHAQGVIRHDI 527  
QY 442 KSDSILLTHDGRVKLSDFGFCQAVSKEVPRKSLVGTPTWMAPELISRLPYGGEVDIWSL 501  
D 528 KSDSILLTHDGRVKLSDFGFCQAVSKEVPRKSLVGTPTWMAPELISRLPYGGEVDIWSL 587  
QY 502 GIMVIMVDGEPYPFNEPPLKAMKMRDNLPRKLNHVKVSPSLKGLFDRLLVRDPAORA 561  
D 588 GIMVIMVDGEPYPFSDSPVQAMKRLRDSPPPKLNKSHKVSPLRDFLERMLVRDPOERA 647  
QY 562 TAAELKHPPFLAKAGPPASIVPLMRQNR 589  
D 648 TAQELLDHFPFLQTLGPECLVPLIQLYR 675

;; TITLE OF INVENTION: Threonine Kinase  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSER: Cooper & Dunham LLP  
;; STREET: 1185 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 11230  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/082,737  
;; FILING DATE:  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: White, John P.  
;; REGISTRATION NUMBER: 0575/55311  
;; REFERENCE/DOCKET NUMBER: 0575/55311  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 278-0400  
;; TELEFAX: (212) 391-0525  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 250 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-082-737-3

Query Match 41.3%; Score 1277; DB 3; Length 250;  
Best Local Similarity 99.6%; Pred. No. 4.5e-75;  
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 324 FIKIGEGSTGIVCIATVRSSGKLVAKMDLKKQORRELLFNEVIMRDYQHENVVMYN 383  
Db 1 FIKIGEGSTGIVCIATVRSSGKLVAKMDLKKQORRELLFNEVIMRDYQHENVVMYN 60  
  
QY 384 SYLVGDELWVMVEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKS 443  
Db 61 SYLVGDELWVMVEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKS 120  
  
QY 444 DSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGI 503  
Db 121 DSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGI 180  
  
QY 504 MVIEMVDGEPYPFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFLLVDRDPAQRATA 563  
Db 181 MVIEMVDGEPYPFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFLLVDRDPAQRATA 240  
  
QY 564 AELLKHPFLA 573  
Db 241 AELLKHPFLA 250

RESULT 11  
US-09-718-032-3  
; Sequence 3, Application US/09718032  
; Patent No. 6667168  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE  
; FILE REFERENCE: 575/55311-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/718,032  
; CURRENT FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: PCT/US99/11341  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 09/082,737

;; PRIOR FILING DATE: 1998-05-21  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 250  
;; TYPE: PRT  
;; ORGANISM: human  
US-09-718-032-3  
  
Query Match 41.3%; Score 1277; DB 4; Length 250;  
Best Local Similarity 99.6%; Pred. No. 4.5e-75;  
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 324 FIKIGEGSTGIVCIATVRSSGKLVAKMDLKKQORRELLFNEVIMRDYQHENVVMYN 383  
Db 1 FIKIGEGSTGIVCIATVRSSGKLVAKMDLKKQORRELLFNEVIMRDYQHENVVMYN 60  
  
QY 384 SYLVGDELWVMVEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKS 443  
Db 61 SYLVGDELWVMVEFLEGGALTDIVTHTRMNEEQIAAACLAVLQALSVLHAQGVHHRDIKS 120  
  
QY 444 DSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGI 503  
Db 121 DSILLTHDGRVKLSDFGCAQVSKVPRKSLVGTPTWMAPELISRLPYGPEVDIWSLGI 180  
  
QY 504 MVIEMVDGEPYPFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFLLVDRDPAQRATA 563  
Db 181 MVIEMVDGEPYPFNEPPLKAMKMRDNLPPRLKNLHKVSPSLKGFLLVDRDPAQRATA 240  
  
QY 564 AELLKHPFLA 573  
Db 241 AELLKHPFLA 250

RESULT 12  
US-08-935-760-2  
; Sequence 2, Application US/08935760A  
; Patent No. 5952217  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Jessica A.  
; APPLICANT: Manly, Susan  
; TITLE OF INVENTION: Recombinant Yeast Cell and Assay Using Same  
; FILE REFERENCE: ON0156sequence  
; CURRENT APPLICATION NUMBER: US/08/935,760A  
; CURRENT FILING DATE: 1997-09-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Rattus exulans  
US-08-935-760-2

Query Match 29.5%; Score 912; DB 2; Length 544;  
Best Local Similarity 35.7%; Pred. No. 3.3e-51;  
Matches 210; Conservative 87; Mismatches 166; Indels 126; Gaps 8;  
  
QY 4 KKKKRVETISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIE-----ESARRPKPLVDP 56  
Db 63 KEKERPEISLPSDFEHTIHVGFDVAVTGFTGIPQWARRLQTSNTKLEQKKNPQAVLD- 121  
  
QY 57 ACITTSIQPGAPKTIVRGSKGAKDGAITLLLDDEFENMVSRTSNLSRRDSPPPPARAQENG 116  
Db 122 -----VLKPYDSKETVNNQKYSFT----- 141  
  
QY 117 MPEBPATTARGPGKAGSRGRFAGHSEAGGSGDERRRAGPKRPKSSREGSGGQESSRD 176  
Db 142 -----SGDKSAHYIAAHQ-----SNTKASEPPLAPPVSEEDDEEEBDD 184  
  
QY 177 KRPLSGPDVGTPOQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGG 236  
Db 185 NEP---PPIVAPRPEHTKS-----IYTRSVESIASPA-----APNKEATPP 223







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:38:51 ; Search time 16.5132 Seconds  
(without alignments)  
1863.563 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGKKRKVEISAPNSFEHR.....LAKAGPPASIVPLMRQNR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3090	100.0	591	PAK4 HUMAN	O96013 homo sapien
2	1731	56.0	719	PAK7 HUMAN	Q9P286 homo sapien
3	1473.5	47.7	681	PAK6 HUMAN	Q9NQU5 homo sapien
4	917	29.7	544	PAK3 RAT	O62829 rattus norv
5	909	29.4	544	PAK3 HUMAN	O75914 homo sapien
6	907	29.4	544	PAK3 MOUSE	Q61036 mus musculus
7	904	29.3	524	PAK2 HUMAN	Q13177 homo sapien
8	900	29.1	524	PAK2 RABIT	Q29502 oryctolagus
9	895	29.0	524	PAK2 RAT	Q64303 rattus norv
10	894	28.9	544	PAK1 RAT	P35465 rattus norv
11	892.5	28.9	545	PAK1 HUMAN	Q13153 homo sapien
12	889.5	28.8	545	PAK1 MOUSE	O88643 mus musculus
13	846.5	27.4	1230	ST20 CANAL	Q92212 candida alb
14	837	27.1	939	ST20 YEAST	Q03497 saccharomyc
15	823.5	26.7	658	PAK1 SCHPO	P50527 schizosacch
16	810	26.2	971	CLA4 CANAL	O14427 candida alb
17	760	24.6	842	CLA4 YEAST	P48562 saccharomyc
18	697	22.6	589	SHK2 SCHPO	Q10056 schizosacch
19	651.5	21.1	655	SKM1 YEAST	Q12469 saccharomyc
20	520	16.8	491	STK3 HUMAN	Q13188 homo sapien
21	512.5	16.6	487	STK3 HUMAN	Q13043 homo sapien
22	509.5	16.5	553	SPAK RAT	O88506 rattus norv
23	498	16.1	471	SID1 SCHPO	O14305 schizosacch
24	497.5	16.1	556	SPAK MOUSE	Q9Z1W9 mus musculus
25	497	16.0	894	PAK3 HUMAN	Q81VH8 homo sapien
26	495.5	16.0	547	SPAK HUMAN	Q9UEW8 homo sapien
27	494	16.0	862	M4K3 RAT	Q92412 rattus norv
28	487.5	15.8	916	TNIK MOUSE	P83510 mus musculus
29	487.5	15.8	1360	TNIK HUMAN	Q9UKE5 homo sapien
30	486	15.7	821	TNIK MOUSE	O61161 mus musculus
31	484.5	15.7	443	ST24 HUMAN	Q9Y660 homo sapien
32	484	15.7	833	M4K1 HUMAN	Q92918 homo sapien
33	478	15.5	669	HPO_DROME	O8T086 drosophila

## RESULT 1

ID	PAK4_HUMAN	STANDARD;	PRT;	591 AA.
AC	O96013; Q9BUJ3;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Serine/threonine-protein kinase PAK 4 (EC 2.7.1.-) (p21-activated kinase 4) (PAK-4).			
DE	kinase 4) (PAK-4).			
GN	PAK4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RN	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	MEDLINE=99043860; PubMed=9822598;			
RX	Abo A., Qu J., Cammarano M.S., Dan C., Fritsch A., Baud V.,			
RA	Belisle B., Minden A.;			
RT	"PAK4, a novel effector for Cdc42Hs, is implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia".;			
RT	EMBO J. 17:6527-6540(1998).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RN	Melnick M.B.;			
RA	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RN	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Eye, Pancreas, and Placenta;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,			
RT	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".;			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-!- FUNCTION: ACTIVATES THE JNK PATHWAY. IMPLICATED IN THE REORGANIZATION OF THE ACTIN CYTOSKELETON AND IN THE FORMATION OF FILOPODIA.			
CC	-!- SUBUNIT: INTERACTS TIGHTLY WITH RAC1.			
CC	CC CDC42/P21 AND WEAKLY WITH RAC1.			

34	477.5	15.5	1308	1	M4K6_MOUSE	Q9Jm52 mus musculus
35	476	15.4	819	1	M4K2_HUMAN	Q12851 h mitogen-a
36	475.5	15.4	1332	1	M4K6_HUMAN	Q8n4c8 homo sapien
37	470.5	15.2	1239	1	M4K4_HUMAN	Q95819 homo sapien
38	469	15.2	846	1	M4K5_HUMAN	Q9y4k4 homo sapien
39	466	15.1	847	1	M4K5_MOUSE	Q8bpm2 mus musculus
40	464	15.0	426	1	ST25_HUMAN	Q00506 homo sapien
41	461	14.9	426	1	ST25_MOUSE	Q922w1 mus musculus
42	461	14.9	827	1	M4K1_MOUSE	P70218 mus musculus
43	456.5	14.8	966	1	STKA_MOUSE	O50598 mus musculus
44	455.5	14.7	1080	1	NRK1_YEAST	P38692 saccharomyc
45	455	14.7	1233	1	M4K4_MOUSE	P97820 mus musculus

## ALIGNMENTS



RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Franks J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leivaeslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund K.C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming I., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 CC -!- FUNCTION: The activated kinase acts on a variety of targets (By  
 CC similarity).  
 CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
 CC CDC42/P21 AND RAC1 (BY SIMILARITY).  
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in brain.  
 CC -!- PTM: Autophosphorylated when activated by CDC42/p21 (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC STE20 subfamily.  
 CC -!- SIMILARITY: Contains 1 CRIB domain.  
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 CC -----  
 DR EMBL; AB040812; BA941194.1; -;  
 DR EMBL; AB033090; BAA86578.1; ALT\_INIT.  
 DR EMBL; AL353612; CAC34367.1; -;  
 DR HSSP; P24941; 1BUH.  
 DR Genew; HGNC:15916; PAK7.  
 DR MIM; 608038; -;  
 DR InterPro; IPR000095; PAKbox/RhoBndng.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 11 24  
 FT CRIB.  
 FT DOMAIN 25 448  
 FT LINKER.  
 FT DOMAIN 449 700  
 FT PROTEIN\_KINASE.  
 FT NP\_BIND 455 463  
 FT ATP (BY SIMILARITY).  
 FT BINDING 478 478  
 FT ATP (BY SIMILARITY).  
 FT ACT\_SITE 568 568  
 FT BY SITE  
 SQ SEQUENCE 719 AA; 80744 MW; 07A12B1EBC4E2A02 CRC64;

Query Match 56.0%; Score 1731; DB 1; Length 719;  
 Best Local Similarity 52.4%; Pred No. 2.1e-59;  
 Matches 393; Conservative 66; Mismatches 126; Indels 156; Gaps 17;  
 QY 1 MFGRKKKEISAPSNFHRVHTGPDQHEQKFTGLPRQMSLIESARPKPLVDPACT 60  
 DB 1 MFGRKKKEISAPSNFHRVHTGPDQHEQKFTGLPRQMSLIESARPKPLVDPACT 60  
 QY 61 STOPGAPKTIIVRGSKGAKGALTLLIDPENMVSRTSLRSDSPPPARA-----R 112  
 DB 61 PQLAPMKTIVRGNKPKCKETSINGLLEDFDNISVTRSLRKSPPPTDQGASSHPGHA 120  
 QY 113 QENGM-----PEEPATTA-----RGG-----PGKA 132  
 DB 121 EENGPIFSQYSSESDDTADYITEKYREKSLYGGDLDPPYRGSHAAKQNGHVMKMHGEA 180  
 QY 133 -----GSRGRFAGH-----SEAG 145  
 DB 181 YYSEVKPLKSDPARFSADYHSHLDSLKPSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA 240  
 QY 146 GSGDERRA-----GP-----EKPCKSREGSGGPOESSRDKPLSGPDVGTGTP-QPA 191  
 DB 241 GTSGGCSLAYSESEWGPSLDDYDRRPPKSSVYNQTSPOPTMR-QKSRSGSLQEPMPMF 299  
 QY 192 GLASGAKLAAGRPFNFY-----PRADTDH-----PSRGAQGEHDAVAPGP 232  
 DB 300 GASAFKTHPGHSHSYNSYTYPRLSEPTMCIPKVDYDRAQMVLPPLSGS-----DTYPRGP 354  
 QY 233 SAGGLAIPOS-----SSSSSRPPTRARGAPSPGLGPHASEPQLAPPACTP----- 278  
 DB 355 A-----KLPOSQSKSGYSSSSHQVPSGYHKA---TLYHHPSLQSSSQYISTASYLSLSL 406  
 QY 279 AAPAVPGPGRSPQEPORVSHEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIA 338  
 DB 407 SSTYPPPSWSSSDQPSRVSHEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIA 466  
 QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENNVEMNSYLVGDELWVWMEFL 398  
 DB 467 TEKHTGQVAVKMDLRKQORRELLFNEVIMRDYHHDNVDMYSSYLVGDELWVWMEFL 526  
 QY 399 EGGALTDIVTHTRMNEQIAAACLAVLQALSVLHAGQVHTRDKSILLTHDGRVKLSD 458  
 DB 527 EGGALTDIVTHTRMNEQIATVCLSVLRALSVLHNGQVHTRDKSILLTHDGRVKLSD 586  
 QY 459 FGFCACQSVKEVPKSLVGTGYWMAPELISRLPYGPEVDIWSLGIWVMDGEPYFNE 518  
 DB 587 FGFCACQSVKEVPKSLVGTGYWMAPEVLSRLPYGTEVDIWSLGIWVMDGEPYFNE 646  
 QY 519 PPLKAMKMRDNLPPRLKNLHKVSPSLKGLFRLDLVLRDPAQRATAAELLKHPFLAKAGPP 578  
 DB 647 PPLQAMRIRDSLPVRVKDLHKVSVLRGLDMLVLRPSQRATAOELLGHPFLKLAGPP 706  
 QY 579 ASIVPLMRQNR 589  
 DB 707 SCIVPLMRQVR 717  
 RESULT 3  
 PAK6\_HUMAN  
 ID PAK6\_HUMAN STANDARD; PRT; 681 AA.  
 AC Q9NQU5;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 6 (EC 2.7.1.-) (p21-activated  
 DE kinase 6) (PAK-6) (PAK-5).  
 OS Homo sapiens (Human).  
 GN PAK6 OR PAK5.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.



DE kinase 3) (PAK-3) (Beta-PAK) (P65-PAK).  
GN PAK3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 37-56.  
RC TISSUE=Brain;  
RX MEDLINE=96027610; PubMed=7559638;  
RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C.,  
RA Lim L.;  
RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated  
RT kinase (PAK) family.";  
RL J. Biol. Chem. 270:25070-25078(1995).  
CC -!- FUNCTION: The activated kinase acts on a variety of targets.  
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3  
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK (BY  
CC SIMILARITY).  
CC -!- TISSUE SPECIFICITY: DETECTED AT HIGH LEVELS IN THE BRAIN AND AT  
CC LOW LEVELS IN THE TESTIS.  
CC -!- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE  
CC EXPRESSION ELSEWHERE.  
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC STE20 subfamily.  
CC -!- SIMILARITY: Contains 1 CRIB domain.  
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CC -----  
DR EMBL; U33314; AAC52268.1; -.  
DR PIR; A57597; A57597.  
DR HSSP; P24941; ICKP.  
DR InterPro; IPR000095; PAKbox/RhoGbinding.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser Thr pkin AS.  
DR InterPro; IPR002290; Ser Thr pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00786; PBD; 1.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot kinase; 1.  
DR SMART; SM00285; PBD; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS50108; CRIB; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation.  
FT DOMAIN 70 83  
FT DOMAIN 84 267  
FT DOMAIN 268 519  
FT NF BIND 274 282  
FT BINDING 297 297  
FT ACT SITE 387 387  
FT ACT SITE 387 387  
FT SEQUENCE 544 AA; 60710 MW; 7B940FC204A2B48B CRC64;  
Query Match 29.7%; Score 917; DB 1; Length 544;  
Best Local Similarity 35.8%; Pred. No. 1.1e-28;  
Matches 211; Conservative 87; Mismatches 165; Indels 126; Gaps 8;  
  
QY 4 KRKKRVEISAPSFHEHVHTGFDQHEQKFGTGLPRWQSLLIE-----ESARPKEPLVDP 56  
DB 63 KEKERPEISLPSDFEHTIHVGFDAVTGFTGPEQMARLLQTSNITKLEQKNPQAVLD- 121

QY 57 ACITSIQPGAPKTIVRGSKGADGALTLTLLDFENNSVTRNSLSRRDSDPPPPARARQENG 116  
DB 122 -----VLKFDYSKETVNNQKYSFT----- 141  
QY 117 MPEEPATTARGGPGKAGSRGRFAGHSEAGGGGDRRRAGPEKRPKSSREGSGGPGQSSRD 176  
DB 142 -----SGDKSAHYIAAHQ-----SNTKTASEPPLAPPVSEDEDEEEEDD 184  
QY 177 KPPLSGPDVGTQPGAGLAKAGRPENTYPRADTDHPSRGAQGEPHDVAENGPSAGG 236  
DB 185 NEP---PPVIAPRPENTKS-----IYTRSVVESIASPA-----APNKEATPP 223  
QY 237 LAIPQSSSSSSRPPTRRGAPSPGLPHASEPOLAPPACTPAAPAVPGPPGPRSPREP 296  
DB 224 SAENANSSLYRNTDR----- 243  
QY 297 QRVSHQFRAALQLVDDPGDPRSYLDFNFKIGEGSTGIVCIATVRSRGLVAVKMDLRK 356  
DB 244 SKMTDEILEKLRSIVSGDPKKYTRFEKIGQAGSTVYVTDIATGQEVAKQNNLQ 303  
QY 357 QQRRELLFNEVIMRDYQHENVVEMVNSVLGDELWVMEFLEGGALTDIVTHTRNNEQ 416  
DB 304 QPKELIINEILLVMRENKPNIVNYLDSVLGDELWVMEYLAGGSLTDVVTETCDEGQ 363  
QY 417 IAAVCLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKSLV 476  
DB 364 IAAVCRECLQALDFLHNSQVHHRDIKSDNLLGMDGSKVLTDFGCAQITPEQSKRSTW 423  
QY 477 GTPYMAPELISRLPYGPEVDIMSLGIMVIMVVDGPPYFNEPPLKAMKIRDLNPPRLK 536  
DB 424 GTPYMAPEVTVTKAYGPKVDIMSLGIMVIMVVDGPPYFNEPPLNENPLRALLYIATNGTPELQ 483  
QY 537 NLHKVPSLKGFLDLLVDDPAQRATAELLKHPFLAKAGPPASIVPLM 585  
DB 484 NPERLSAVFRDFLNCLEMDVDVRRGSAKELLQHPFLKAKPLSLPLI 532  
  
RESULT 5  
ID\_PAK3\_HUMAN STANDARD; PRT; 544 AA.  
AC 075914;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated  
DE kinase 3) (Beta-PAK) (Oligophrenin-3).  
GN PAK3 OR OPHN3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND DISEASE.  
RX MEDLINE=98400251; PubMed=9731525;  
RA Allen K.M., Gleeson J.G., Bagrodia S., Partington M.W.,  
RA Macmillan J.C., Cerione R.A., Mulley J.C., Walsh C.A.;  
RT "PAK3 mutation in nonsyndromic X-linked mental retardation.";  
RL Nat. Genet. 20:25-30(1998).  
CC -!- FUNCTION: The activated kinase acts on a variety of targets.  
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3  
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN POSTMITOTIC NEURONS OF THE  
CC DEVELOPING AND POSTNATAL CEREBRAL CORTEX AND HIPPOCAMPUS.  
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.  
CC -!- DISEASE: Defects in PAK3 are the cause of non-specific X-linked  
CC nonsyndromic mental retardation type 30 (MRX30) [MIM:300142].  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC STE20 subfamily.  
CC -!- SIMILARITY: Contains 1 CRIB domain.  
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KW Transferase; Serine/threonine-protein kinase; ATP-binding;

```
KW Phosphorylation.
FT DOMAIN 74 87 CRIB.
FT 88 248 LINKER.
FT DOMAIN 249 499 PROTEIN KINASE.
FT NP_BIND 255 263 ATP (BY SIMILARITY).
FT BINDING 278 278 ATP (BY SIMILARITY).
FT ACT_SITE 367 367 BY SIMILARITY.
FT CONFLICT 90 90 A -> T (IN REF. 2).
FT CONFLICT 150 150 L -> P (IN REF. 2).
FT CONFLICT 225 225 P -> T (IN REF. 2).
FT CONFLICT 329 329 G -> R (IN REF. 2).
FT CONFLICT 338 338 T -> TA (IN REF. 1).
SQ SEQUENCE 524 AA; 58004 MW; DB2A7A72BB6B1072 CRC64;

Query Match 29.3%; Score 904; DB 1; Length 524;
Best Local Similarity 35.0%; Pred. No. 3.3e-28;
Matches 211; Conservative 94; Mismatches 136; Indels 162; Gaps 13;

QY 4 KKKRVEISAPSNFHRVHTGPDQHEQKFTGLPROMQSLIE-----ESARRPKPLVDP 56
Db 67 KEKERPEISPPSDFEHTIHVGFDVAVTGFTGMPEQWARLLQTSNITKLEQKNPQAVLD- 125
QY 57 ACITSIQCAPKTIIVRGSKGADGALTLLDDEFENSVTRSNLRD--SPPPPARAQE 114
Db 126 -----VLKPYD-----SNTVKQKYLSTFP-----EK 147
QY 115 NGMPE-EPATTARGGPKAGSRGRFAGHSEAGGSDRRRAGPEKPKSSREGSGGPQES 173
Db 148 DGLPSGTALNAG-----TEA-----PAVTEEDDDDET 178
QY 174 SDRKPLSGPDVGTQPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHDPVAPNGPS 233
Db 179 A-----PPVIAPRDPHTKS-----IYTRSVID-PVPAPVGDSh----- 210
QY 234 AGGLAIPOSSSSSRPRTRAGAPSGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQ 293
Db 211 -----VDGAASKSLDKQ 221
QY 294 REPQVSHEQFRAALQLVVDGPDPSYLDNFKIGEGSTGIYCIATVRSSGKLVAKKMD 353
Db 222 KKKPKMTDEEINKEKURTVISIGDPKKYTRYEKIQGAGSTVFTADVALGQEVAKQIN 281
QY 354 LRQQRRELFNEVIMRDYQHENVVYNSLVGDELVMVMEFLGGALTDIVTHRN 413
Db 282 LQKQPKKELJINEILVMKELKNPNIWNFLDSYLVGDELFWMEYLAGGLSDVVTETCD 341
QY 414 EQIIAAVCLAVLQALSVLHAQGVHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRK 473
Db 342 EAQIAAVCRECIQALEFLHANQVHRIKSDNVLGMESGVKLTDGFCQAQITPEQSKRS 401
QY 474 SLVGTPTYNMAPELISRLPYGPEVDIWSLGIWMIEMVDGEPYFNBPPLKAMKWRDNLPP 533
Db 402 TWVGTPYNMAPEVTRKAGPKVDIWSLGIWMIEMVEGEPYFNENPLRALYLIATNGTP 461
QY 534 RLKLNHKVSPSLKGLFRLDRVPAQARATAELLKHPFLAKAGGPASIVPL-----MR 586
Db 462 ELONPEKLSPIFRDFLNRCLMDVEKRGSAKELLQHPFLKAKPLSLPLIIMAAKEAMK 521
QY 587 QNR 589
Db 522 SNR 524
```

## RESULT 8

```
PAK2_RABIT
ID PAK2_RABIT STANDARD; PRT; 524 AA.
AC Q29502;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated
kinase 2) (PAK-2) (Gamma-PAK) (p21-activated protein kinase 1)
```

```
DE (PAK1).
GN PAK2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198078; PubMed=8626411;
RA Jakobi R., Chen C., Tuazon P.T., Traugh J.A.;
RT "Molecular cloning and sequencing of the cytosolic G protein-
activated protein kinase PAK 1."
RL J. Biol. Chem. 271:6206-6211(1996).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U46915; AAC48537.1; -.
CC HSP; P24941; ICRP.
CC InterPro; IPR000095; PAKbox/RhoGndng.
CC InterPro; IPR000719; Prot Kinase.
CC InterPro; IPR008271; Ser Thr pkin AS.
CC InterPro; IPR002290; Ser_thr_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00786; PBD; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR0109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00285; PBD; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS0108; CRIB; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00111; PROTEIN KINASE DOM; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 74 87 CRIB.
FT DOMAIN 88 248 LINKER.
FT DOMAIN 249 500 PROTEIN KINASE.
FT NP_BIND 255 263 ATP (BY SIMILARITY).
FT BINDING 278 278 ATP (BY SIMILARITY).
FT ACT_SITE 368 368 BY SIMILARITY.
SQ SEQUENCE 524 AA; 58027 MW; 39D71020EADFCA CRC64;

Query Match 29.1%; Score 900; DB 1; Length 524;
Best Local Similarity 34.4%; Pred. No. 4.6e-28;
Matches 207; Conservative 95; Mismatches 140; Indels 160; Gaps 12;

QY 4 KKKRVEISAPSNFHRVHTGPDQHEQKFTGLPROMQSLIE-----ESARRPKPLVDP 56
Db 67 KEKERPEISPPSDFEHTIHVGFDVAVTGFTGMPEQWARLLQTSNITKLEQKNPQAVLD- 125
QY 57 ACITSIQCAPKTIIVRGSKGADGALTLLDDEFENSVTRSNLRD--SPPPPARAQE 114
Db 126 -----VLKPYD-----SNTVKQKYLSTFP-----EK 147
QY 115 NGMPEEPATTARGGPKAGSRGRFAGHSEAGGSDRRRAGPEKPKSSREGSGGPQES 174
Db 148 DGFPs-----GAPALNTKVSETSAVVTEDD 173
QY 175 RKRPLSGPDVGTQPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEHDPVAPNGPS 234
```

Db 174 DDBE-AAPPVIAPRPDHTKS-----IYTRVID-PIPAVGDSDH----- 210  
 QY 235 GGLAIPQSSSSSRPPTFRAGSPGVGLPHASEPOLAPPACTPAAPAVGPPGPRSPQR 234  
 Db 211 -----VDSGAKSSDK----- 222  
 QY 295 EPQVRSHEQFRAALQLVVDGDPSPRSYDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMDL 354  
 Db 223 KTKMTDEEMKLRITVSGDPKKYTRYEKLGQASGVFTATDVALGQFVAIQINL 282  
 QY 355 RKQORRELLFNEVIMRDYQHENVYMSYLVGDELWVMEFLEGALTDIVTHRMNE 414  
 Db 283 QKQPKKELIINEILVMKELKPNVFNFLSDYLVGDELWVMEYLAGSLTDVVTETCME 342  
 QY 415 EQIAAACLAVLQALSVLHAQGVTHRDIKSDSIILTHDGRVKLSDFGFCQVSKVEVPKRS 474  
 Db 343 AQIAAACLAVLQALSVLHAQGVTHRDIKSDSIILTHDGRVKLSDFGFCQVSKVEVPKRS 474  
 QY 475 LVGTPYMAPELISRLPYGPEVDIWSLGIWVIMVDEGPEPPYFNEPPLKAMKMDRLNLP 533  
 Db 403 MVGTPYMAPEVTRKAYGKVDIWSLGIWVIMVDEGPEPPYFNEPPLKAMKMDRLNLP 533  
 QY 535 LKMLHVKVPSLKGFLDRLLVDRPAQRATAELLKHPFLAKAGPPASTIVPL-----MRQ 587  
 Db 463 LQNPVKLSPIFRDLNCLMDVKEKRSKAKELLQHPFLKLPKLSLTLPLMAAKEMKS 522  
 QY 588 NR 589  
 Db 523 NR 524

RESULT 9  
 PAK2 RAT  
 ID PAK2 RAT STANDARD; PRT; 524 AA.  
 AC Q6403;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated  
 DE kinase 2) (PAK-2) (Gamma-PAK) (P62-PAK).  
 GN PAK2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Brain, and Testis;  
 RX MEDLINE=96064759; PubMed=7592896;  
 RA Teo M., Manser E., Lim L.;  
 RT "Identification and molecular cloning of a p21cdc42/rac1-activated  
 RT serine/threonine kinase that is rapidly activated by thrombin in  
 RT platelets.";  
 RL J. Biol. Chem. 270:26690-26697(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Mabel T.;  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: The activated kinase acts on a variety of targets.  
 CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
 CC CDC42/P21 AND RAC1.  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.  
 CC -!- PTM: Autophosphorylated when activated by CDC42/p21.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC STE20 subfamily.  
 CC -!- SIMILARITY: Contains 1 CRIB domain.  
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 CC -----  
 DR EMBL; S80221; AAB35608.1; -;  
 DR EMBL; U35345; AAA79064.1; -;  
 DR HSSP; P24941; 1CKP.  
 DR InterPro; IPR000095; PAKbox/Rhobndng.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 74 87 CRIB.  
 FT DOMAIN 88 248 LINKER.  
 FT DOMAIN 249 500 PROTEIN KINASE.  
 FT NP\_BIND 255 263 ATP (BY SIMILARITY).  
 FT BINDING 278 278 ATP (BY SIMILARITY).  
 FT ACT\_SITE 368 368 BY SIMILARITY.  
 SQ SEQUENCE 524 AA; 57960 MW; A3F2FEB81C8D4294 CRC64;  
 Query Match 29.0%; Score 895; DB 1; Length 524;  
 Best Local Similarity 34.5%; Pred. No. 7.2e-28;  
 Matches 208; Conservative 92; Mismatches 141; Indels 162; Gaps 12;  
 QY 4 KRKKRVEISAPSNFHRVHTGFDQHEQKFTGLPROMQSLIE-----ESARPKPLVDP 56  
 Db 67 KEKERPEISPPSDFEHTIHVGFDAVTGETGPEQWARLLQTSNITKLOKKNPQAVLD- 125  
 QY 57 ACITSIQPGAPKTIVRGSKGAKDGALTLLDDEFNNMVSVTRNSLRD--SPPPPAPARQE 114  
 Db 126 -----VLKFDY-----SNTVKQKYLSETPP-----EK 147  
 QY 115 NGMPE-EPATTARGGPKAGSRGRFAGHSEAGGSGDRRAGPEKPKSRSRGSGPQES 173  
 Db 148 DGFPSTGTPALNTKGS-----IYTRVID-----PIPA 205  
 QY 174 SRDKRPLSGFDVGTPOAGLASKAKLAGRPENTYPRADTDHPSRGAQGEHPDVAENGPS 233  
 Db 172 DDDDED-AAPPVIAPRPDHTKS-----IYTRVID-----PIPA 205  
 QY 234 AGGLAIPQSSSSSRPPTFRAGSPGVGLPHASEPOLAPPACTPAAPAVGPPGPRSPQ 293  
 Db 206 VGDSNVDSGAKSSDK-----Q 221  
 QY 294 REPQVRSHEQFRAALQLVVDGDPSPRSYDNFIKIGEGSTGIVCIATVRSRSGKLVAVKMD 353  
 Db 222 KKKAKMTDEEMKLRITVSGDPKKYTRYEKLGQASGVFTATDVALGQFVAIQIN 281  
 QY 354 LRQQRRELLFNEVIMRDYQHENVYMSYLVGDELWVMEFLEGALTDIVTHRMN 413  
 Db 282 LQKQPKKELIINEILVMKELKPNVFNFLSDYLVGDELWVMEYLAGSLTDVVTETCMD 341  
 QY 414 EQIAAACLAVLQALSVLHAQGVTHRDIKSDSIILTHDGRVKLSDFGFCQVSKVEVPKRS 473  
 Db 342 EAQIAAACLAVLQALSVLHAQGVTHRDIKSDSIILTHDGRVKLSDFGFCQVSKVEVPKRS 473  
 QY 474 LVGTPYMAPELISRLPYGPEVDIWSLGIWVIMVDEGPEPPYFNEPPLKAMKMDRLNLP 533  
 Db 402 MVGTPYMAPEVTRKAYGKVDIWSLGIWVIMVDEGPEPPYFNEPPLKAMKMDRLNLP 533  
 QY 535 LKMLHVKVPSLKGFLDRLLVDRPAQRATAELLKHPFLAKAGPPASTIVPL-----MR 586

Db 462 ELONPEKLSPIRDFLNRCLNDEMVEKRSKELLQHPFLKLAQLSLTPLILAKEAMK 521

QY 587 QNR 589

Db 522 SNR 524

RESULT 10

PAK1 RAT STANDARD; PRT; 544 AA.

AC P35465; Q62934;

DT 01-JUN-1994 (Rel. 29, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated kinase 1) (PAK-1) (P68-PAK) (Alpha-PAK) (Protein kinase MUK2).

GN PAK1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1] \_TaxID=10116;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=94150588; PubMed=8107774;

RA Manser E., Leung T., Salihuddin H., Zhao Z.-S., Lim L.;

RT "A brain serine/threonine protein kinase activated by Cdc42 and Rac1".

RL Nature 367:40-46(1994).

RN [2]

RP REVISIONS.

RA Zhao Z.-S.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I., Ohno S.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP TISSUE SPECIFICITY

RX MEDLINE=96027610; PubMed=7559638;

RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C., Lim L.;

RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) family".

RL J. Biol. Chem. 270:25078(1995).

CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS. LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED GTPASES TO THE UNK MAP KINASE PATHWAY.

CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/p21 AND RAC1 (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BRAIN. WITH HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH MOTOR FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.

CC -!- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE EXPRESSION ELSEWHERE.

CC -!- PTM: Autophosphorylated when activated by CDC42/p21.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. STE20 subfamily.

CC -!- SIMILARITY: Contains 1 CRIB domain.

CC

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CC

CC EMBL; U23443; AAB95646.1; -.

CC EMBL; U49953; AAB61533.1; -.

CC PDB; 1EOA; 14-SEP-00.

DR InterPro; IPR000095; PAKbox/RhoBndng.

DR InterPro; IPR000719; Prot. kinase.

DR InterPro; IPR008271; Ser thr\_pkin AS.

DR InterPro; IPR002290; Ser thr\_pkinase.

DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00786; PBD; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR PRODOM; PD000001; Prot. kinase; 1.

DR SMART; SM00285; PBD; 1.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00108; CRIB; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; 3D-structure.

KW Phosphorylation; 3D-structure.

FT DOMAIN 75 88 CRIB

FT DOMAIN 89 268 LINKER.

FT DOMAIN 269 520 PROTEIN\_KINASE.

FT NP\_BIND 275 283 ATP (BY SIMILARITY).

FT BINDING 298 298 ATP (BY SIMILARITY).

FT ACT\_SITE 388 388 BY SIMILARITY.

SQ SEQUENCE 544 AA; 60577 MW; 93BE32D8222F5B7B CRC64;

Query Match 28.9%; Score 894; DB 1; Length 544;

Best Local Similarity 36.9%; Pred. No. 8.1e-28;

Matches 216; Conservative 82; Mismatches 165; Indels 122; Gaps 11;

QY 4 KKKVEIISAPSNFHRVHTGFDQHEQKFTGLPROMQSLIESARRPKPLVDPACTISIQ 63

Db 68 KEKERPEISLPSDFEHTIHVGFDVATGFTGMPQWALLQTSN----- 111

QY 64 PGAPKTIIVRGSKGAKDGALTLLIDFENMSVTRNSLRDSDPPPARAFQENMPPEPAT 123

Db 112 -----ITKSEQKNPQAVLDVLEFYNSKKT-SNSQYMS----- 144

QY 124 TARGFGKAGSRGRFAGHSEAGGSGDRRRAGPEKRPKSSRGSGPQSSDKPLSGP 183

Db 145 -----FTDKSAEDYNSNTLNV-----KTVSETPAVPPVSEDE---DD 180

QY 184 DVGTPQAGLASAKLAAGRPENT---YPRADTDHPSRGAQGEHDVAENGFSAAGLAIP 240

Db 181 DDATPPP-----VIAPRPEHTKSVYTRSVI-----EPLPVTPT----- 213

QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPGSPRSPQREFQVS 300

Db 214 RDVATSPISPTENNTTP-----PDALTTRNT-----EKQKKPKWS 248

QY 301 HEQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIICIAIVRSRSGKLVAVKMDLRKQOR 360

Db 249 DEEILEKLSRISVSGDPKKKYTRFEKIGQASGTVYTAMDVATGQEVAIKQNNLOQPKK 308

QY 361 ELLFNEVIMRDYQIHENVVMYNSVLGDELWVMEFLGGALTDLVTHTRNNEEQIAAV 420

Db 309 ELIINELLWMRENKPNIVNYLDLSVLGDELWVMEYLAGSLTDVVTETCDEGQIAAV 368

QY 421 CLAVLQALSVLHAQGVIIHRDIKSDSILLTHDGRVKLSDFGCAQVSKEYPRRKLKLVGTPY 480

Db 369 CRECLQALEFLHSNQVIHRDIKSDNILLGMDGSKVLTDFGCAQITPEQSKSTWVGTPY 428

QY 481 WNAPELISRLPYGPEVDWISLGIMVEMWDGPPFPNEPPLKAMKMRNLNLPRLKHLHK 540

Db 429 WNAPEVVTTKAYGPKVDIWSLGIMAEIMEGPPYINENPLRALYLIATNGTPELQNPKEK 488

QY 541 VSPSLKGFUDRLILVRDPAQRATAAELLKHPFLKAKAGPPASIVPLM 585

Db 489 LSAIFRDLNRCLEMDVEKRSKELLQHPFLKIAKPLSLTFLI 533

RESULT 11

PAK1 HUMAN

ID \_PAK1\_HUMAN

AC Q13153; Q13567;

DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.37) (p21-activated  
DE kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK).  
GN PAK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=97199447; PubMed=9395435;  
RX Sells M.A., Knaus U.G., Bagrodia S., Ambrose D.M., Bokoch G.M.,  
RA Chernoff J.;  
RA "Human p21-activated kinase (Pak1) regulates actin organization in  
RT mammalian cells.";  
RL Curr. Biol. 7:202-210 (1997).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=96398842; PubMed=8805275;  
RA Brown J.L., Stowers L., Baer M., Trejo J., Coughlin S., Chant J.;  
RT "Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinase  
RT pathway.";  
RL Curr. Biol. 6:598-605 (1996).  
RN [3]  
RN FUNCTION, AND INTERACTION WITH CDC2L1 AND CDC2L2.  
RX MEDLINE=22651041; PubMed=12624090;  
RA Chen S., Yin X., Zhu X., Yan J., Ji S., Chen C., Cai M., Zhang S.,  
RA Zong H., Hu Y., Yuan Z., Shen Z., Gu J.;  
RT "The C-terminal kinase domain of the p34cdc2-related PITSURE protein  
RT kinase (p110C) associates with p21-activated kinase 1 and inhibits  
RT its activity during anoikis";  
RL J. Biol. Chem. 278:20029-20036 (2003).  
CC -!- FUNCTION: The activated kinase acts on a variety of targets.  
CC Likely to be the GTPase effector that links the Rho-related  
CC GTPases to the JNK MAP kinase pathway. Activity inhibited in cells  
CC undergoing apoptosis, potentially due to binding of CDC2L1 and  
CC CDC2L2.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- COFACTOR: Magnesium.  
CC -!- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound  
CC CDC42/p21 and RAC1. Binds to the caspase-cleaved p110 isoform of  
CC CDC2L1 and CDC2L2, p110C, but not the full-length proteins.  
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC STE20 subfamily.  
CC -!- SIMILARITY: Contains 1 CRIB domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U24152; AAC65441.1; --  
CC EMBL; U51120; AAC50590.1; --  
CC FIR; G01773; G01773.  
CC PDB; 1F3M; 29-NOV-00.  
CC Genew; HGNC:8590; PAK1.  
CC MIM; 602590; --  
CC GO; GO:0007254; P-JNK cascade; TAS.  
CC GO; GO:0006468; P-protein amino acid phosphorylation; TAS.  
CC InterPro; IPR000095; PAKBox/Phobond.  
CC InterPro; IPR000719; Prot kinase.  
CC InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
CC InterPro; IPR002290; Ser\_Thr\_pkinase.  
CC InterPro; IPR001245; Tyr\_pkinase.  
CC Pfam; PF00786; PBD; 1.  
CC Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00285; PBD; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR PROSITE; PS00108; CRIB; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
KW Apoptosis; Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW phosphorylation; 3D-structure.  
FT DOMAIN 75 88  
FT DOMAIN 89 269  
FT DOMAIN 270 521  
FT NP\_BIND 276 284  
FT BINDING 299 299  
FT ACT\_SITE 389 389  
FT MUTAGEN 107 107  
FT CONFLICT 26 26  
FT CONFLICT 237 237  
FT CONFLICT 379 379  
FT CONFLICT 503 503  
SQ SEQUENCE 545 AA; 60661 MW; 14A1E70E6480CD7E CRC64;  
  
Query Match 28.9%; Score 892.5; DB 1; Length 545;  
Best Local Similarity 36.9%; Pred. No. 9.2e-28;  
Matches 216; Conservative 82; Mismatches 166; Indels 121; Gaps 11;  
  
QY 4 KRKRVEISAPSNFHRVITGPDQHEQKFTGLPROMOSLIEESARRPKPLVDPACTISIQ 63  
DB 68 KEKERDEISLPSDFEHTIHVGFDVAVTGFTGMPEQWARLLQTSN----- 111  
QY 64 PGAKPIVRGSGAKGKALTLLIDEPENMSVTRNSLRDSDPPPARAQENGMPPEPAT 123  
DB 112 -----ITKSEQKNQPAVLVDVLEFYNSKKT-SNSQKYS----- 144  
QY 124 TARGPGKAGSRGFAGHSEAGSGDRRRAGPEKPKSRREGSGPQESSRDRPLSGP 183  
DB 145 -----FTDKSAEDVNSSNALNV-----KAVSETPAVPVSEDED---DDD 181  
QY 184 DVGTPQAGLASAKLAAGRPNW---YPRADTHPSRGAQGEPHDVAENGPSAGGLAIP 240  
DB 182 DDAATPPP-----VIAPRPEHTKSVYTRSVI-----EPLPVTPT----- 214  
QY 241 QSSSSSRSPTRRAGAPSPGLPHASEQLAPPACTPAAPVPGPPGPRSPQRPQVS 300  
DB 215 RDAVTSPISTENNTTP-----PDALTRNT-----EKOKKKPKMS 249  
QY 301 HQQFRAALQLVVDGDPDRSYLDNFIKIGEGSTGIVCIATVRSGLVAVKMDLRKQRR 360  
DB 250 DBEILEKLRSIVSGDPKKKYTRFKIGQSGASTVYTMVATGQEVAKQNNLQOQPKK 309  
QY 361 ELLFNQVIMRDYQHNVMYNSYLVDGLVWMEFLGGALTDIVTTRNNEEQIAAV 420  
DB 310 ELIINEILVMRRNKPNINIVYLDLSVLVDGLVWMEYLAGGSLTDVVTETCMDEGQIAV 369  
QY 421 CLAVLQALSVLHAQGVHHRDIKSDSILLTHDGRVKLSDFGCAQVSKVEPRKSLVGTPT 480  
DB 370 CRECQLALEFLHSNQVHHRDIKSDNILLGMDGSKVLTDFGCAQITPQSKSKSTWGTPT 429  
QY 481 WMAPELISRLPYGPEVDIWSLGIWIMVMDGPPPFNEPPLKAMKIMRDNLPRLKNLHK 540  
DB 430 WMAPEVTVTRKAYGPKVDIWSLGIWIMVMDGPPPFNEPPLKAMKIMRDNLPRLKNLHK 489  
QY 541 VPSLSKGFELDRLLVDRDPAQATAAELLKHPFLAKAGPPASIVPLM 585  
DB 490 LSAIFRDFLNRLCLMDVKEKRSKELLQHQFLKIAKPLSLTFLI 534  
  
RESULT 12  
PAK1\_MOUSE  
ID\_FAKI\_MOUSE STANDARD; PRT; 545 AA.  
AC O88643;  
DT 15-DEC-1998 (Rel. 37, Created)







CC CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC CC STE20 subfamily.  
CC CC -!- SIMILARITY: Contains 1 CRIB domain.  
CC CC -----  
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC CC the European Bioinformatics Institute. There are no restrictions on its  
CC CC use by non-profit institutions as long as its content is in no way  
CC CC modified and this statement is not removed. Usage by and for commercial  
CC CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC CC -----  
CC CC EMBL; M94719; AAA35111.1; -  
CC CC EMBL; L04655; AAA35038.1; -  
CC CC EMBL; L04655; AAA35039.1; -  
CC CC EMBL; U11581; AAB69747.1; -  
CC CC PIR; S28394; S28394.  
CC CC HSP; O63450; 1A06.  
CC CC GerMOnline; 139274; -  
CC CC SGD; S0000999; STE20.  
CC CC GO; GO:0000131; C:incipient bud site; IDA.  
CC CC GO; GO:0005937; C:shmoo tip; IDA.  
CC CC GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.  
CC CC GO; GO:000282; P:bud site selection; IMP.  
CC CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
CC CC InterPro; IPR000035; PAKbox/RhoBndg.  
CC CC InterPro; IPR000719; Prot\_kinase.  
CC CC InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
CC CC InterPro; IPR002290; Ser\_thr\_pkinase.  
CC CC InterPro; IPR001245; Tyr\_pkinase.  
CC CC Pfam; PF00786; PBD; 1.  
CC CC Pfam; PF00669; pkinase; 1.  
CC CC PRINTS; PR00109; TYRKINASE.  
CC CC ProDom; PD000001; Prot\_kinase; 1.  
CC CC SMART; SM00285; PBD; 1.  
CC CC SMART; SM00220; S\_TKc; 1.  
CC CC PROSITE; PS0108; CRIB; 1.  
CC CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
CC CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
CC CC PROSITE; PS00108; PROTEIN KINASE ST; 1.  
CC CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
CC CC Pheromone response; Phosphorylation.  
CC CC PT DOMAIN 337 350 CRIB.  
CC CC FT DOMAIN 620 871 PROTEIN KINASE.  
CC CC FT NP BIND 626 634 ATP (BY SIMILARITY).  
CC CC FT BINDING 649 649 ATP (BY SIMILARITY).  
CC CC FT ACT SITE 739 739 BY SIMILARITY.  
CC CC FT CONFLICT 19 19 N -> S (IN REF. 2).  
CC CC FT CONFLICT 134 134 I -> M (IN REF. 2).  
CC CC FT CONFLICT 271 271 P -> S (IN REF. 2).  
CC CC SEQENCE 939 AA; 102362 MW; 69C1C12F5B87733C CRC64;  
CC CC Query Match 27.1%; Score 837; DB 1; Length 939;  
CC CC Best Local Similarity 32.3%; Pred. No. 1.8e-25;  
CC CC Matches 208; Conservative 98; Mismatches 191; Indels 146; Gaps 13;  
CC CC -----  
CC CC 9 VEISAPNFVHVTGFDQHEQKTEGLPRQWOSLIESARRKPLVDPACTISIQCAPK 68  
CC CC 335 LRISTPYNAKHIVGVDSKTGYTGLPEWEKLLTSSGI----- 374  
CC CC -----  
CC CC 69 TIVRGSKAGDGLTLLIDPE-NMSVTRNSLRDSDPPPPARARQNGMPEEPATTARG 127  
CC CC 375 -----SKREQQNQAVNDIVKFQDVTEING-----EDKMFKTNTTT-G 414  
CC CC -----  
CC CC 128 GPGKAGSRGRFAGHSEAGGGSGDRRRRAGPEKPKSREGSGGPGPESRDKPLS----- 181  
CC CC 415 LPGS-----PQVST-----PPANSFNKFPPTSDSHN 441  
CC CC -----  
CC CC 182 -GPDVGTGPQAGLASGAKLAAGRPENTYPRADTDHPSRGAQGEHDVAPNGPSAGGLAIP 240  
CC CC 442 YGSRGTGTPMNHVMS-----PTLNTDSSANGKFIISRPAKPPSSASAP 488  
CC CC -----  
CC CC 241 -----QSSSSSSRPPTTRGAPSPGVLGPHAS-----BFLQAPP----- 274

Db 489 IIKSPVWNSAANVSPLKQTHAPTTPNRTSPNRSISRNATLKKEQPLPPIPTPKSKTSP 548  
QY 275 -----ACTPAAPAVPGPPRSPQRPQVSHE-----QFRAALQ 309  
Db 549 IISTAHTQQVAQSPKAPAQETVTFTSKPAQASLSKELNEKKKEERRRKKQLYAKLN 608  
QY 310 LVVDPGDPSPYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLURKQORRELLNEVVI 369  
Db 609 EICSGDPSFTKYANLVKIQGASGGVYAYEIGTGVSVVAIKQMNLEKQPKKELIINEIV 668  
QY 370 MRDYQHEVNVEMYSYLVGDELWVMEFEGGALTDIVTHTMNEEQIAAACLAVLQALS 429  
Db 669 MKGSXHPNIVNFIDSYVLKGLWVIMEYMEGSLTDVVTHCILTEGQIGAVCRETLISGLE 728  
QY 430 VLHAQGVHHRDIKSDSIILLTHDGRVYKLSDFGCAOVSKVEPRPKSLVGTGYWMAPELISR 489  
Db 729 FLHSGVLRHDIKSDNILLSMEGDIKLTDFGCAQINELNKRKTTVMGTGYWMAPEVVS 788  
QY 490 LPYGEVDIWSLGINVIMVGDGEPYFNEPPIKAMKMRDNPRIKLNHVKVSPSLKGL 549  
Db 789 KEYGPKVDIWSLGINMIEMIEGEPYLNETPLRALYLIATNGTPTKLKEPENLSSSLKKFL 848  
QY 550 DLLLVDPQAQATAAELLKHPFLAK-AGPPASIVPLMRQNRTR 591  
Db 849 DWCLCVPEDRASATELLHDEYITETAANSSSLAPLVKLARLK 891  
  
RESULT 15  
PAK1\_SCHPO STANDARD; PRT; 658 AA.  
ID PAK1\_SCHPO  
AC P50527;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Serine/threonine-protein kinase pak1/shk1 (EC 2.7.1.-).  
GN PAK1 OR SHK1 OR ORB2 OR SPBCL604.14C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96112805; PubMed=8846783;  
RA Ohtsue S., Miller P.J., Johnson D.I., Creasy C.L., Sells M.A.,  
RA Bagrodia S., Forsburg S.L., Chernoff J.,  
RT "Fission yeast pak1+ encodes a protein kinase that interacts with  
RL Cdc42p and is involved in the control of cell polarity and mating.";  
RL EMBO J. 14:5908-5919(1995).  
[2]  
RP SEQUENCE FROM N.A.  
RA Marcus S.,  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Cellins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
RA Collins S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds R., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,  
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,



CC		
ENBL;	U22371; AAC49125.1; --	
ENBL;	AL034433; CAA22347.1; --	
ENBL;	L41552; AAB52609.1; --	
PIR;	S60170; S60170.	
PIR;	T39500; T39500.	
HSP;	Q00534; IBI8.	
GeneDB_Spomc;	SPBC1604.14c; --	
InterPro;	IPR000095; PAKbox/RhoBndng.	
InterPro;	IPR000719; Prot_kinase.	
InterPro;	IPR008271; Ser_thr_pkin_AS.	
InterPro;	IPR002290; Ser_thr_pkinase.	
InterPro;	IPR001245; Tyr_pkinase.	
Pfam;	PF00786; PBD; 1.	
Pfam;	PF00069; pkinase; 1.	
PRINTS;	PR00109; TYRKINASE.	
ProDom;	PD000001; Prot_kinase; 1.	
SMART;	SM00285; PBD; 1.	
SMART;	SM00220; S_TKC; 1.	
PROSITE;	PS00108; CRIB; 1.	
PROSITE;	PS00107; PROTEIN_KINASE_ATP; 1.	
PROSITE;	PS00011; PROTEIN_KINASE_DOM; 1.	
PROSITE;	PS00108; PROTEIN_KINASE_ST; 1.	
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;	
Phosphorylation.		
FT DOMAIN	147 160	CRIB.
FT FT	85 88	POLY-SER.
FT DOMAIN	234 237	POLY-SER.
FT DOMAIN	246 249	POLY-SER.
FT DOMAIN	263 267	POLY-SER.
FT DOMAIN	386 637	PROTEIN_KINASE.
FT NP_BIND	392 400	ATP (BY SIMILARITY).
FT BINDING	415 415	ATP (BY SIMILARITY).
ACT_SITE	505 505	BY SIMILARITY.
FT CONFLICT	492 495	GLOH -> LYSD (IN REF. 1).

Search completed: September 29, 2004, 18:02:01  
Job time : 21.5132 secs

Search completed: September 29, 2004, 18:02:01  
Job time : 21.5132 secs

Blank

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:57:52 ; Search time 6.54412 Seconds  
(without alignments)  
1308.205 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	303	67.0	540	2 T19956	hypothetical prote
2	303	67.0	542	2 T19952	hypothetical prote
3	277	61.3	544	2 S40482	serine/threonine-s
4	277	61.3	545	2 G01773	p21-activated prot
5	276	61.1	544	2 A57597	beta-p21-activated
6	269	59.5	544	2 I49376	p21 activated kina
7	266	58.8	622	2 T15467	hypothetical prote
8	265.5	58.7	525	2 S58682	protein kinase, p2
9	256	56.6	1230	2 T18256	probable serine/th
10	256	56.6	1230	2 T18259	probable serine/th
11	255	56.4	939	2 S28394	probable serine/th
12	235.5	52.1	378	2 T26684	hypothetical prote
13	231.5	51.2	842	2 S60402	protein kinase CLA
14	231	51.1	658	2 T39500	serine/threonine-s
15	227	50.2	558	2 S60170	protein kinase Pak
16	220.5	48.8	589	2 T38086	serine/threonine-p
17	203.5	45.0	655	2 S51884	probable protein k
18	177.5	39.3	819	2 A53714	protein kinase (EC
19	167.5	37.1	829	2 T29372	hypothetical prote
20	154	34.1	1102	2 JC6316	probable protein k
21	153	33.8	836	2 B96716	probable serine/th
22	151.5	33.5	1401	2 T39225	MAP kinase kinase
23	148.5	33.1	545	2 T37748	hypothetical prote
24	148.5	32.9	652	2 T39722	serine/threonine p
25	146.5	32.4	1192	2 T18611	probable serine/th
26	146.5	32.4	1246	2 G89287	protein H39E23.1 [
27	146	32.3	1233	2 T30989	serine/threonine p
28	145.5	32.2	1075	2 T27623	hypothetical prote
29	145.5	32.2	1080	2 T27622	hypothetical prote

30	145.5	32.2	1314	2 S19488	probable membrane
31	145	32.1	471	2 T39232	probable serine th
32	144.5	32.0	348	2 T37521	Caz+/calmodulin-de
33	143	31.6	653	2 T34356	hypothetical prote
34	142.5	31.5	690	2 C96572	protein F12M16.4 [
35	141.5	31.3	1051	1 JW0051	serine/threonine-s
36	141.5	31.3	1579	2 S59801	protein kinase SSK
37	138.5	30.6	312	2 T38525	serine/threonine p
38	137.5	30.4	1062	2 S46367	protein kinase CDC
39	136	30.1	415	2 JQ2251	calcium/calmodulin
40	135.5	30.0	460	2 S58882	protein kinase Cds
41	135.5	30.0	883	2 A96662	hypothetical prote
42	135	29.9	1206	2 T34021	protein kinase SK2
43	135	29.9	1231	2 T18532	serine/threonine p
44	135	29.9	1233	2 T14157	serine/threonine p
45	133	29.4	1097	2 F96538	hypothetical prote

ALIGNMENTS

RESULT 1

T19956

hypothetical protein C45B11.1b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000

C:Accession: T19956

R;McMurray, A.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19202

A:Accession: T19956

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-540 <WIL>

A:Cross-references: EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C45B11.1b

A:Experimental source: clone C45B11

C:Genetics:

A:Gene: CESP:C45B11.1b

A:Map position: 5

A:Introns: 13/2; 62/3; 104/2; 231/3; 367/2; 468/3

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 67.0%; Score 303; DB 2; Length 540;

Best Local Similarity 67.4%; Pred. No. 2.1e-20;

Matches 60; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENNVNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60

Db 284 KQORRELFNEVIMRDYRHENNVNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 343

QY 61 QIANVCLAVLQALAVLHAQGVHSDIKTD 89

Db 344 QIATISQVLGALDFUARKVIHRDKSD 372

RESULT 2

T19952

hypothetical protein C45B11.1a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000

C:Accession: T19952

R;McMurray, A.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19202

A:Accession: T19952

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-542 <WIL>

A:Cross-references: EMBL:Z74029; PIDN:CAA98429.1; GSPDB:GN00023; CESP:C45B11.1a

A:Experimental source: clone C45B11

C:Genetics:

A:Gene: CESP:C45B11.1a

A:Map position: 5

A; Introns: 13/2; 62/3; 104/2; 233/3; 369/2; 470/3  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

Query Match 67.0%; Score 303; DB 2; Length 542;  
Best Local Similarity 67.4%; Pred. No. 2.1e-20;  
Matches 60; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 286 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 345

QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89  
DB 346 QIATISRQVLGALDFLHARKVHRIKSD 374

RESULT 3  
S40482  
serine/threonine-specific protein kinase (EC 2.7.1.1) - rat  
C; Species: Rattus norvegicus (Norway rat)  
C; Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C; Accession: S40482  
R; Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.  
Nature 367, 40-46, 1994  
A; Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.  
A; Reference number: S40482; MUID:94150588; PMID:8107774  
A; Accession: S40482  
A; Molecule type: mRNA  
A; Residues: 1-544 <MAN>  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F; 267-520/Domain: protein kinase homology <KIN>  
F; 275-283/Region: protein kinase ATP-binding motif

Query Match 61.3%; Score 277; DB 2; Length 544;  
Best Local Similarity 58.4%; Pred. No. 5e-18;  
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 304 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDG 363

QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89  
DB 364 QIAAVCRECLQALEFLHSNQVHRIKSD 392

RESULT 4  
G01773  
p21-activated protein kinase - human  
C; Species: Homo sapiens (man)  
C; Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 24-Sep-1999  
C; Accession: G01773  
R; Chernoff, J.  
submitted to the EMBL Data Library, April 1995  
A; Reference number: G08374  
A; Accession: G01773  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
A; Residues: 1-545 <CHE>  
A; Cross-references: EMBL:U24152; NID:G780805; PIDN:AAA65441.1; PID:G780806  
C; Genetics:  
A; Gene: Pak1  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
F; 268-521/Domain: protein kinase homology <KIN>

Query Match 61.3%; Score 277; DB 2; Length 545;  
Best Local Similarity 58.4%; Pred. No. 5.1e-18;  
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 305 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDG 364

A; Introns: 13/2; 62/3; 104/2; 233/3; 369/2; 470/3  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

Query Match 67.0%; Score 303; DB 2; Length 542;  
Best Local Similarity 67.4%; Pred. No. 2.1e-20;  
Matches 60; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 286 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 345

QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89  
DB 346 QIATISRQVLGALDFLHARKVHRIKSD 374

RESULT 3  
S40482  
serine/threonine-specific protein kinase (EC 2.7.1.1) - rat  
C; Species: Rattus norvegicus (Norway rat)  
C; Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C; Accession: S40482  
R; Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.  
Nature 367, 40-46, 1994  
A; Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.  
A; Reference number: S40482; MUID:94150588; PMID:8107774  
A; Accession: S40482  
A; Molecule type: mRNA  
A; Residues: 1-544 <MAN>  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F; 267-520/Domain: protein kinase homology <KIN>  
F; 275-283/Region: protein kinase ATP-binding motif

Query Match 61.3%; Score 277; DB 2; Length 544;  
Best Local Similarity 58.4%; Pred. No. 5e-18;  
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 304 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDG 363

QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89  
DB 364 QIAAVCRECLQALEFLHSNQVHRIKSD 392

RESULT 4  
G01773  
p21-activated protein kinase - human  
C; Species: Homo sapiens (man)  
C; Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 24-Sep-1999  
C; Accession: G01773  
R; Chernoff, J.  
submitted to the EMBL Data Library, April 1995  
A; Reference number: G08374  
A; Accession: G01773  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
A; Residues: 1-545 <CHE>  
A; Cross-references: EMBL:U24152; NID:G780805; PIDN:AAA65441.1; PID:G780806  
C; Genetics:  
A; Gene: Pak1  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
F; 268-521/Domain: protein kinase homology <KIN>

Query Match 61.3%; Score 277; DB 2; Length 545;  
Best Local Similarity 58.4%; Pred. No. 5.1e-18;  
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 305 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDG 364

QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89  
DB 365 QIAAVCRECLQALEFLHSNQVHRIKSD 393

RESULT 5  
A57597  
beta-p21-activated protein kinase - rat  
N; Alternate names: beta-PAK  
C; Species: Rattus norvegicus (Norway rat)  
C; Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 24-Sep-1999  
C; Accession: A57597  
R; Manser, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L.  
J. Biol. Chem. 270, 25070-25078, 1995  
A; Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) family.  
A; Reference number: A57597; MUID:96027610; PMID:7559638  
A; Accession: A57597  
A; Status: preliminary  
A; Molecule type: mRNA  
A; Residues: 1-544 <MAN>  
A; Cross-references: GB:U33314; NID:G1039424; PIDN:AAC52268.1; PID:G1039425  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C; Keywords: ATP  
F; 266-519/Domain: protein kinase homology <KIN>  
F; 274-282/Region: protein kinase ATP-binding motif

Query Match 61.1%; Score 276; DB 2; Length 544;  
Best Local Similarity 58.4%; Pred. No. 6.2e-18;  
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 303 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDG 362

QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89  
DB 363 QIAAVCRECLQALDFLHSNQVHRIKSD 391

RESULT 6  
I49376  
P21 activated kinase-3 - mouse  
C; Species: Mus musculus (house mouse)  
C; Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 24-Sep-1999  
C; Accession: I49376  
R; Bagrodia, S.; Taylor, S.J.; Creasy, C.L.; Chernoff, J.; Cerione, R.A.  
J. Biol. Chem. 270, 22731-22737, 1995  
A; Title: Identification of a mouse p21Cdc42/Rac activated kinase.  
A; Reference number: I49376; MUID:96032693; PMID:7559398  
A; Accession: I49376  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
A; Residues: 1-544 <RES>  
A; Cross-references: EMBL:U39738; NID:G1079713; PIDN:AAC52354.1; PID:G1079714  
C; Genetics:  
A; Gene: mPAK-3  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C; Keywords: ATP  
F; 266-519/Domain: protein kinase homology <KIN>  
F; 274-282/Region: protein kinase ATP-binding motif

Query Match 59.5%; Score 269; DB 2; Length 544;  
Best Local Similarity 57.3%; Pred. No. 2.7e-17;  
Matches 51; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 303 QQPKKELIINEILVMRENKPNINVLDSYLVGDELWVMEYLAGGSLTDVVTCTMDG 362

QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89  
DB 363 QIAAVCRECLQALDFLHSNQVHRIKSD 391

```
RESULT 7
T15467
hypothetical protein C09B8.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 19-May-2000
C:Accession: T15467
R:Stelljes, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid C09B8.
A:Reference number: S61138
A:Accession: T15467
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-622 <STE>
A:Cross-references: EMBL:U29612; NID:9868273; PID:9868279; PIDN:AAA68805.1; CESP:C09B8.7
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C09B8.7
A:Introns: 107/1; 142/3; 192/1; 260/3; 291/3; 481/1; 505/3; 546/3; 570/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
Query Match 58.8%; Score 266; DB 2; Length 622;
Best Local Similarity 56.8%; Pred. No. 6e-17;
Matches 50; Conservative 18; Mismatches 20; Indels 0; Gaps 0;
QY 2 QORRELLFNEVIMRDYRHENVVEMNSYLVDGLWVMEFLGGGALTDIVTHTRMNEEQ 61
DB 381 QPKKELIINEILVMRKGNINIVYLDVLVDGLWVMEYLGGSLTDVVTEQMEDGI 440
QY 62 IAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 441 IAAVCEVLQALEFLHSRHHVHRDIKSD 468
RESULT 8
S58682
protein kinase, p21-activated (EC 2.7.1.1) - human
N:Alternate names: protein kinase PAK65; S6/H4 kinase
C:Species: Homo sapiens (man)
C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 24-Sep-1999
C:Accession: S58682; S55258; S55304; S58690; A57441
R:Sells, M.; Knause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.
submitted to the EMBL Data Library, April 1995
A:Description: Human p21-activated protein kinases regulate actin organization in mammal
A:Reference number: S58682
A:Accession: S58682
A:Molecule type: DNA
A:Residues: 1-525 <SEL>
A:Cross-references: EMBL:U24153; NID:g780807; PIDN:AAA65442.1; PID:g780808
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.
EMBO J. 14, 1970-1978, 1995
A:Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation i
A:Reference number: S55258; MUID:95262637; PMID:7744004
A:Accession: S55258
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'MEETQKSNLEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525
A:Accession: S55304
A:Molecule type: protein
A:Residues: 402-418 <MAW>
R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.
EMBO J. 14, 4385, 1995
A:Reference number: S58690; MUID:96016211; PMID:7556080
A:Contents: erratum
A:Accession: S58690
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-30 <MAP>
R:Benner, G.E.; Dennis, P.B.; Masaracchia, R.A.
J. Biol. Chem. 270, 2121-21128, 1995
A:Title: Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular an
```

```
A:Reference number: A57441; MUID:95403344; PMID:7673144
A:Accession: A57441
A:Molecule type: protein
A:Residues: 197-216; 402, 'S', 404-409 <BEN>
A:Experimental source: placenta
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin
F:247-501/Domain: protein kinase homology <KIN>
F:255-263/Region: protein kinase ATP-binding motif
F:197,402/Binding site: phosphate (Ser) (covalent) #status predicted
Query Match 58.7%; Score 265.5; DB 2; Length 525;
Best Local Similarity 57.8%; Pred. No. 5.5e-17;
Matches 52; Conservative 18; Mismatches 19; Indels 1; Gaps 1;
QY 1 KQORRELLFNEVIMRDYRHENVVEMNSYLVDGLWVMEFLGGGALTDIVTHTRMNEE 59
DB 284 KQPKKELIINEILVMRKGNINIVYLDVLVDGLWVMEYLGGSLTDVVVTACMDE 343
QY 60 EQIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 344 AQIAAVCRECLQALEFLHANQVHHRDIKSD 373
RESULT 9
T18256
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - yeast (Candida albicans)
C:Species: Candida albicans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18256
R:Leberer, E.; Marcus, D.; Broadbent, I.D.; Clark, K.L.; Dignard, D.; Ziegelbauer, K.; Sc
proc. Natl. Acad. Sci. U.S.A. 93, 13217-13222, 1996
A:Title: Signal transduction through homologs of the Ste20p and Ste7p protein kinases car
A:Reference number: Z18843; MUID:97075145; PMID:8917571
A:Accession: T18256
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1230 <LEB>
A:Cross-references: EMBL:L47210; NID:g2276410; PID:g2286042; PIDN:AAB65439.1
C:Keywords: phosphotransferase; serine/threonine-specific protein kinase
Query Match 56.6%; Score 256; DB 2; Length 1230;
Best Local Similarity 50.6%; Pred. No. 1e-15;
Matches 45; Conservative 21; Mismatches 23; Indels 0; Gaps 0;
QY 1 KQORRELLFNEVIMRDYRHENVVEMNSYLVDGLWVMEFLGGGALTDIVTHTRMNEE 60
DB 989 QQPKKELIINEILVMKGGSHPNIVFIDSYLLKGLDILWIMEYMEGGSLTDIVTHSVMTG 1048
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 1049 QIGVVCRETLLKGLKFLHSKGVHHRDIKSD 1077
RESULT 10
T18259
serine/threonine protein kinase homolog - yeast (Candida albicans)
C:Species: Candida albicans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
C:Accession: T18259
R:Kohler, J.R.; Fink, G.R.
Proc. Natl. Acad. Sci. U.S.A. 93, 13223-13228, 1996
A:Title: Candida albicans strains heterozygous and homozygous for mutations in mitogen-ac
A:Reference number: Z11118; MUID:97075146; PMID:8917572
A:Accession: T18259
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1230 <KOH>
A:Cross-references: EMBL:U73457; NID:g1657953; PID:g1737181; PIDN:AAB38875.1
C:Genetics:
Query Match 56.6%; Score 256; DB 2; Length 1230;
```



A;Cross-references: SGD:S0005242; MIPS:YNL298w  
 A;Map position: 14L  
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; pleckstrin repeat homology  
 F;544-825/Domain: protein kinase homology <KIN>

Query Match 51.1%; Score 231.5; DB 2; Length 842;  
 Best Local Similarity 40.4%; Pred. No. 1e-13;  
 Matches 36; Conservative 28; Mismatches 25; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYL-VGDELWVWVEFLEGGALTDIV----- 52  
 DB 600 KQPKKEFLVNEILVMKSHHKNVFNFDITFFYKSELMMVMYMRGGSLEVTNTLTSEG 659

QY 53 -TTRMNEEQIAAACLAVLQALVLAHQGVTHSDIKTD 89  
 DB 660 NSHSPLEPQIAYIVRETQGLKFLHDKHIIHRDIKSD 697

## RESULT 14

T39500  
 serine/threonine-specific protein kinase (EC 2.7.1.1-) paki-shk1 - fission yeast (Schizosaccharomyces pombe)  
 N;Alternate names: Ste20 homologous protein kinase 1  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000

R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, December 1998

A;Reference number: Z21859

A;Accession: T39500

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-658 <BEC>

A;Cross-references: EMBL:AL034433; PIDN:CAA22347.1; GSPDB:GN000666; SPDB:SPBC1604.14C  
 A;Experimental source: strain 972h-; cosmid C1604

R;Marcus, S.

submitted to the EMBL Data Library, April 1997

A;Reference number: Z22999

A;Accession: T45523

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-658 <MAR>

A;Cross-references: EMBL:L41552; PIDN:AAB52609.1

C;Genetics:

A;Gene: shk1; SPBC1604.14C

A;Map position: 1

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
 C;Keywords: hydrolase; phosphotransferase; signal transduction

Query Match 51.1%; Score 231; DB 2; Length 658;  
 Best Local Similarity 40.4%; Pred. No. 1e-13;  
 Matches 36; Conservative 28; Mismatches 25; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYL-VGDELWVWVEFLEGGALTDIVTHTRNNEE 60  
 DB 421 QQPKKEFLVNEILVMKSHHKNVFNFDITFFYKSELMMVMYMRGGSLEVTNTLTSEG 480

QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89  
 DB 481 QIAAICKETLEGLHENGIVHRDIKSD 509

## RESULT 15

S60170

protein kinase Pak1 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 24-Sep-1999

C;Accession: S60170

R;Ottillie, S.; Miller, P.J.; Johnson, D.I.; Creasy, C.L.; Sells, M.A.; Bagrodia, S.; For

EMBO J. 14, 5908-5919, 1995

A;Title: Fission yeast paki(+) encodes a protein kinase that interacts with Cdc42p and

A;Reference number: S60170; MUID:96112805; PMID:8846783

A;Accession: S60170

A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-658 <OTT>

A;Cross-references: EMBL:U22371; NID:g1122910; PIDN:AAC49125.1; PID:g1122911  
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
 C;Keywords: ATP

F;384-637/Domain: protein kinase homology <KIN>  
 F;392-400/Region: protein kinase ATP-binding motif

Query Match 50.2%; Score 227; DB 2; Length 658;  
 Best Local Similarity 39.3%; Pred. No. 2.4e-13;  
 Matches 35; Conservative 29; Mismatches 25; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVMYNSYL-VGDELWVWVEFLEGGALTDIVTHTRNNEE 60  
 DB 421 QQPKKEFLVNEILVMKSHHKNVFNFDITFFYKSELMMVMYMRGGSLEVTNTLTSEG 480

QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89  
 DB 481 QIAAICKETLEGLHENGIVHRDIKSD 509

Search completed: September 29, 2004, 18:05:38  
 Job time : 7.54412 secs



Blank

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 17:41:57 ; Search time 20.1559 Seconds  
(without alignments)  
1393.197 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVIIHSIDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rviro:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	443	98.0	407	11	Q8K0U2 mus musculus
2	443	98.0	593	11	Q8BTW9 mus musculus
3	443	98.0	593	11	Q80Z97 mus musculus
4	436	96.5	240	4	Q8NCH5 homo sapien
5	436	96.5	467	4	Q9ULS8 homo sapien
6	436	96.5	483	4	Q8NDE3 homo sapien
7	436	96.5	501	4	Q8N4E1 homo sapien
8	421	93.1	650	13	Q90W62 xenopus lae
9	409	90.5	229	11	Q9CS71 mus musculus
10	407	90.0	719	11	Q8C015 mus musculus
11	402	88.9	719	4	Q8BT93 homo sapien
12	399	88.3	719	11	Q8BVB0 mus musculus
13	366	81.0	639	5	Q9VXE5 drosophila
14	366	81.0	639	5	Q960J8 drosophila
15	366	81.0	639	5	Q96372 drosophila
16	303	67.0	540	5	Q9U3M1 caenorhabdi

17	303	67.0	542	5	Q18637	Q18637 caenorhabdi
18	283	62.6	704	5	Q9V113	Q9V113 drosophila
19	283	62.6	704	5	Q24190	Q24190 drosophila
20	279	61.7	704	5	Q24213	Q24213 drosophila
21	277	61.3	447	4	Q86W79	Q86W79 homo sapien
22	277	61.3	553	4	Q75561	Q75561 homo sapien
23	277	61.3	577	13	Q803Z0	Q803Z0 brachydanio
24	276	61.1	410	4	Q8WVK5	Q8WVK5 homo sapien
25	276	61.1	544	4	Q9P0J8	Q9P0J8 homo sapien
26	276	61.1	544	11	Q8K1R6	Q8K1R6 mus musculus
27	276	61.1	559	4	Q7Z3Z8	Q7Z3Z8 homo sapien
28	276	61.1	559	6	Q7YQL4	Q7YQL4 pan troglod
29	276	61.1	559	6	Q7YQL3	Q7YQL3 pongo pygma
30	276	61.1	559	11	Q8K1R5	Q8K1R5 mus musculus
31	276	61.1	564	13	Q8AXB4	Q8AXB4 xenopus lae
32	274	60.6	524	11	Q9QYU0	Q9QYU0 rattus norv
33	274	60.6	524	11	Q8CIN4	Q8CIN4 mus musculus
34	273	60.4	525	13	Q57318	Q57318 xenopus lae
35	273	60.4	527	13	Q9PW62	Q9PW62 xenopus lae
36	272	60.2	540	4	Q9Y6B5	Q9Y6B5 homo sapien
37	270	59.7	517	13	Q8AW67	Q8AW67 brachydanio
38	266	58.8	300	5	Q86GT9	Q86GT9 caenorhabdi
39	266	58.8	523	5	Q86GU0	Q86GU0 caenorhabdi
40	266	58.8	569	5	Q22041	Q22041 caenorhabdi
41	266	58.8	572	5	Q94133	Q94133 caenorhabdi
42	266	58.8	572	5	Q17850	Q17850 caenorhabdi
43	262	58.0	914	3	Q7Z8E9	Q7Z8E9 magnaporthe
44	261	57.7	517	13	Q919C2	Q919C2 xenopus lae
45	257.5	57.0	644	3	Q9HEW5	Q9HEW5 cryptococcu

## ALIGNMENTS

### RESULT 1

Q8K0U2 PRELIMINARY; PRT; 407 AA.  
AC Q8K0U2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN PAK4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retina;  
RA Strausberg R;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC030389; AAH30389.1; -;  
DR MGD; MGI:1917834; Pak4.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR SMART; SM00219; TyrK; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
FT Hypothetical protein; ATP-binding; Transferase.  
SQ NON\_TER  
SQ SEQUENCE 407 AA; 44339 MW; 921689734DF9D710 CRC64;  
Query Match 98.0%; Score 443; DB 11; Length 407;

Best Local Similarity 97.8%; Pred. No. 1.2e-43;  
Matches 87: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	KQORRELLFNENVIMRDRYHENVVMYNSYLVGDELWVVMFELEGGALTDIVHTRNNEE	60
Db	172	KQORRELLFNENVIMRDRYHENVVMYNSYLVGDELWVVMFELEGGALTDIVHTRNNEE	231
Qy	61	QIAAVCLAVLQALAVLHAQGVHSIDIKTD	89
Db	232	QIAAVCLAVLQALAVLHAQGVHRIKSD	260

```

RESULT 2
Q8BTW9
ID Q8BTW9 PRELIMINARY; PRT; 593 AA.
AC Q8BTW9;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Ssine/threonine-protein kinase PAK 4 (Similar to
DE P21(CDKN1A)-activated kinase 4).
DE PAK4 OR 5730488LO7RIK.
GN Mus musculus (Mouse).
OS OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RT Nature 420:563-573(2002).

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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDPJ databases.
EMBL; AK088512; BAC40396.1; -
EMBL; BC048238; AHA48238.1; -
MED; MGI-1917834; Pak4
GO; GO:0005534; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000095; PAKbox/RhoGndg.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00786; PBD; 1.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKc; 1.
SMART; SM00219; TyPKc; 1.
PROSITE; PS00108; CRIB; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Kinase.
SO SEQUENCE 593 AA: 64632 MW: 4AFA91DD73D4C6D5 CRC64;

	Query Match	98.0%;	Score 443;	DB 11;	Length 593;
	Best Local Similarity	97.8%;	Pred. No. 1.8e-43;		
	Matches	87;	Conservative	1;	Mismatches 43;
					Indels 0; Gaps 0
Qy	1	KQORLELFNEVIMRDYRHNVMYMSYLVGDELVWVMEFLEGALTDIVTHTRMNEE	60		
ph	358	KQORPEFLFNEVIMRDYRHNVMYMSYLVGDELVWVMEFLEGALTDIVTHTRMNEE	417		

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89

418 QIAAVCLAVLQALAVLHAQGVIRDIKSD 446

Db

RESULT 3

Q80297

ID Q80297 PRELIMINARY; PRT; 593 AA.

AC Q80297;

DT 01-JUN-2003 (TEMBLrel. 24, Created)

DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)

DE P21-activated protein kinase 4.

DE Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_Taxid=10090;

CC [1]

RN SEQUENCE FROM N.A.

RP RP

RC STRAIN=BALB/C;

EC MEDLINE=22526742; PubMed=12529371;

RA Lu Y., Pan Z.Z., Devaux Y., Ray P.;

RA "p21-activated Protein Kinase 4 (PAK4) Interacts with the Keratinocyte

RT Growth Factor Receptor and Participates in Keratinocyte Growth Factor-

RT mediated Inhibition of Oxidant-Induced Cell Death.";

RL J. Biol. Chem. 278.10374-10380(2003).

DR EMBL; AY1217016; AAC61496.1; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000095; PAKbox/RhoBndng.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_pkinase.

DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00786; PBD; 1.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00285; PBD; 1.

DR SMART; SM00220; S\_TKC; 1.

DR SMART; SM00219; TYRK; 1.

DR PROSITE; PS0108; CRIB; 1.

DR PROSITE; PS0107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR Kinase.

KW

SEQ SEQUENCE 593 AA; 64566 MW; D7B3BD36706B4AF4 CRC64;

Query Match 98.0%; Score 443; DB 11; Length 593;

Best Local Similarity 97.8%; Pred. No. 1.8e-43;

Match 87. Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	KQQRRELFNEVIMRDYRHENVVMNSYLVGDELWVMEFLGGALTDIVTTRMNEE	60
Db	358	KQQRRELFNEVIMRDYRHENVVMNSYLVGDELWVMEFLGGALTDIVTTRMNEE	417
QY	61	QIAVCLAVLQALAVLHAQGVHDIKTD	89
Db	418	QIAVCLAVLQALAVLHAQGVHDIKSD	446

RESULT	ID	Q8NCH5	PRELIMINARY;	PRT;	240 AA.
Q8NCH5					
AC	Q8NCH5;				
DT	01-OCT-2002	(TRENBLrel. 22, Created)			
DT	01-OCT-2002	(TRENBLrel. 22, Last sequence update)			
DT	01-OCT-2003	(TRENBLrel. 25, Last annotation update)			
DE	Hypothetical protein FLJ90247.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Isocrai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,				

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,  
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
 RT "NEDO human cDNA sequencing project.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK074728; F:ATP binding; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyRKc; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 KW Hypothetical protein; ATP-binding; Transferase.  
 SQ SEQUENCE 240 AA; 27332 MW; E3C686288D4913B6 CRC64;

Query Match 96.5%; Score 436; DB 4; Length 240;  
 Best Local Similarity 95.5%; Pred. No. 4.1e-43;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 60  
 |||||  
 DB 5 KQORRELLFNEVIMRDYQHENVNEMNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 64

QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89  
 |||||  
 DB 65 QIAAVCLAVLQALVLAHQGVHSDIKTD 93

## RESULT 5

Q9ULS8  
 ID Q9ULS8 PRELIMINARY; PRT; 467 AA.  
 AC Q9ULS8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein KIAA1142 (Fragment).  
 GN KIAA1142  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20039618; PubMed=10574461;  
 RA Hirosewa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;  
 RT "Characterization of cDNA clones selected by the GeneMark analysis  
 from size-fractionated cDNA libraries from human brain.";  
 RL DNA Res 6:329-336(1999).  
 DR EMBL; AB032968; BAA86456.1; -.  
 DR HSSP; Q63450; 1A06.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000095; PAKbox/RhoGndg.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS50108; CRIB; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE\_DOM; 1.  
 KW Hypothetical protein; ATP-binding; Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 467 AA; 51464 MW; EC342B8F5C5E3940 CRC64;

Query Match 96.5%; Score 436; DB 4; Length 467;  
 Best Local Similarity 95.5%; Pred. No. 9.2e-43;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 60  
 |||||  
 DB 232 KQORRELLFNEVIMRDYQHENVNEMNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 291

QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89  
 |||||  
 DB 292 QIAAVCLAVLQALVLAHQGVHSDIKTD 320

## RESULT 6

O8NDE3  
 ID Q8NDE3 PRELIMINARY; PRT; 483 AA.  
 AC Q8NDE3;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DKP2F547G182.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Wiemann S.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL834236; CAD38914.1; -.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000095; PAKbox/RhoGndg.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyRKc; 1.  
 DR PROSITE; PS50108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE\_DOM; 1.  
 KW Hypothetical protein; ATP-binding; Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 483 AA; 52787 MW; 8976E3BF0B8818B6 CRC64;

Query Match 96.5%; Score 436; DB 4; Length 483;  
 Best Local Similarity 95.5%; Pred. No. 9.6e-43;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 60  
 |||||  
 DB 248 KQORRELLFNEVIMRDYQHENVNEMNSYLVDGLWVMEFLEGGALTDIVTHTRMNEE 307

QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89  
 |||||  
 DB 308 QIAAVCLAVLQALVLAHQGVHSDIKTD 336

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RESULT 7
Q8N4E1 PRELIMINARY; PRT; 501 AA.
AC Q8N4E1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN cDNA 5730488L07 gene.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Lung;
RP SEQUENCE FROM N.A.
RA Strusberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC034511; AAH34511.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKG; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 501 AA; 5490 MW; 6E86240CEB5E79D CRC64;

Query Match 96.5%; Score 436; DB 4; Length 501;
Best Local Similarity 95.5%; Pred. No. 1e-42; Indels 0; Gaps 0;
Matches 85; Conservative 3; Mismatches 1;

QY 1 KQORRELFNEVIMRDYRHENVYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
Db 266 KQORRELFNEVIMRDYRHENVYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 325

QY 61 QIAAVCLAVLQALVHAQGVHSDIKTD 89
Db 326 QIAAVCLAVLQALVHAQGVHSDIKTD 354

RESULT 8
Q90W62 PRELIMINARY; PRT; 650 AA.
AC Q90W62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PAKS protein.
GN PAKS.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RC TISSUE=Oocyte;
RP SEQUENCE FROM N.A.
RA Cau J., Faure S., Delsert C., Morin N.;
RT "A novel xenopus p21 activated kinase expressed in brain.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A277826; CAC40979.1; -.

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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/RhoGndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKG; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 650 AA; 73736 MW; 9274DC6CADC4A081 CRC64;

Query Match 93.1%; Score 421; DB 13; Length 650;
Best Local Similarity 89.9%; Pred. No. 8e-41; Indels 0; Gaps 0;
Matches 80; Conservative 7; Mismatches 2;

QY 1 KQORRELFNEVIMRDYRHENVYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
Db 415 KQORRELFNEVIMRDYRHENVYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 474

QY 61 QIAAVCLAVLQALVHAQGVHSDIKTD 89
Db 475 QIATVCSVLKALSVLHAQGVHSDIKSD 503

RESULT 9
Q9CS71 PRELIMINARY; PRT; 229 AA.
AC Q9CS71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 5730488L07Rik protein (fragment).
GN PAK4 OR 5730488L07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085860; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017713; BAB30889.1; -.
DR HSSP; Q63450; 1A06.
DR MGD; MGI:1917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

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DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 229 AA; 25896 MW; D9CF2CA73CED941E CRC64;

Query Match 90.5%; Score 409; DB 11; Length 229;  
 Best Local Similarity 97.6%; Pred. No. 5.9e-40;  
 Matches 80; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 LFNEVIMRDYRHENVVEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAVCL 67  
 Db 1 LFNEVIMRDYRHENVVEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAVCL 60  
 QY 68 AVLQALAVLHAQGVTHSDIKTD 89  
 Db 61 AVLQALAVLHAQGVTHSDIKSD 82

RESULT 10  
 Q8C015 PRELIMINARY; PRT; 719 AA.  
 AC Q8C015; (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 5.  
 GN 2900083L08RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK032593; BAC27939.1; -;  
 DR MGD; MGI:1920334; 2900083L08RIK.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000095; PAKbox/RhoGndng.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser thr pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S.TKC; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 SQ SEQUENCE 719 AA; 80948 MW; 5E16D2318C238C8D CRC64;

Query Match 90.0%; Score 407; DB 11; Length 719;  
 Best Local Similarity 87.8%; Pred. No. 4e-39;  
 Matches 78; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVVEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60  
 Db 484 KQORRELFNEVIMRDYRHENVVEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 543  
 QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
 Db 544 QIATVCLSVLRAVLSVHLNQGVTHSDIKSD 572

RESULT 11  
 Q8TB93 PRELIMINARY; PRT; 719 AA.  
 AC Q8TB93; (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE P21(CDKN1A)-activated kinase 7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC024179; AAH24179.1; -;  
 DR HSSP; P24941; 1BUH.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000095; PAKbox/RhoGndng.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser thr pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S.TKC; 1.  
 DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 KW ATP-binding; Kinase; Transferase.  
 SQ SEQUENCE 719 AA; 80794 MW; 536CB5DE65DA9FC3 CRC64;

Query Match 88.9%; Score 402; DB 4; Length 719;  
 Best Local Similarity 86.5%; Pred. No. 1.6e-38;  
 Matches 77; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 KQORRELFNEVIMRDYRHENVVEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 60  
 Db 484 KQORRELFNEVIMRDYRHENVVEMNSYLVGDELWVMEFLEGGALTDIVTHTRMNEE 543  
 QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89  
 Db 544 QIATVCLSVLRAVLSVHLNQGVTHSDIKSD 572

RESULT 12  
 Q8VB0 PRELIMINARY; PRT; 719 AA.  
 AC Q8VB0; (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 5.  
 GN 2900083L08RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK079080; BAC37528.1; --  
DR MGI; MGI:1920334; 2900083L08Rik.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000095; PAKbox/RhoGndng.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00786; PBD; 1.  
DR Pfam; PF00669; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00285; PBD; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyTKc; 1.  
DR PROSITE; PS50108; CRIB; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
SQ SEQUENCE 719 AA; 80967 MW; FLE33DCB8C39875B CRC64;  
Query Match 88.3%; Score 399; DB 11; Length 719;  
Best Local Similarity 86.5%; Pred. No. 3.5e-38;  
Matches 77; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
QY 1 KQORELLFNEVIMRDYRHENVVMYNSYLVGDELWVMELEGALTDIVTTRMNEE 60  
Db 484 KQORELLFNEVIMRDYRHENVVMYNSYLVGDELWVMELEGALTDIVTTRMNEE 543  
QY 61 QIAAVCLAVLQALVHLAQGVTHSDIKTD 89  
Db 544 QIATVCLSLKALSYLHNGQVTHRIKSD 572  
RESULT 13  
Q9VXE5 PRELIMINARY; PRT; 639 AA.  
AC Q9VXE5; Q9TYH2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CG19592 protein (p21 activated kinase related protein).  
GN MBT OR CG18582.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jafarli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferrieria S., Frise E., Galie R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jialik M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RT "Sequencing of Drosophila melanogaster genome."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RT "Annotation of Drosophila melanogaster genome."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99035549; PubMed=9811608;  
RA Melzig J., Rein K.H., Schaefer U., Pfister H., Jaekle H.,  
RA Heisenberg M., Raabe T.;  
RT "A protein related to p21-activated kinase (PAK) that is involved in  
RT neurogenesis in the Drosophila adult central nervous system."  
RL Curr. Biol. 8:1223-1226 (1998).



```
DR EMBL; AE003502; AAF48629.2; -
DR EMBL; AJ011578; CAA09699.1; -
DR FlyBase; FBgn0025743; mbt.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/Rhobndng.
DR InterPro; IPR000719; Ser_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 639 AA; 69620 MW; 414D217F0AEBC1C6 CRC64;

Query Match 81.0%; Score 366; DB 5; Length 639;
Best Local Similarity 78.7%; Pred. No. 2.4e-34;
Matches 70; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVVMYNSYLVGDELWVMVEFEGGALTDIVTHTRNNEE 60
DB 403 KQORRELFNEVIMRDYRHENVVMYNSYLVGDELWVMVEFEGGALTDIVTHSRMDEE 462
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 463 QIATVCKQCLKALAYLHQSQGVHRIKSD 491

RESULT 14
Q960J8 PRELIMINARY; PRT; 639 AA.
AC Q960J8;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE LD47563P.
GN MBT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Pargass V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AY052023; AAK93447.1; -.
DR HSSP; P24941; 1BUH.
DR FlyBase; FBgn0025743; mbt.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/Rhobndng.
DR InterPro; IPR000719; Ser_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
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DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 639 AA; 69592 MW; 2145317F0AE8F554 CRC64;

Query Match 81.0%; Score 366; DB 5; Length 639;
Best Local Similarity 78.7%; Pred. No. 2.4e-34;
Matches 70; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVVMYNSYLVGDELWVMVEFEGGALTDIVTHTRNNEE 60
DB 403 KQORRELFNEVIMRDYRHENVVMYNSYLVGDELWVMVEFEGGALTDIVTHSRMDEE 462
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 463 QIATVCKQCLKALAYLHQSQGVHRIKSD 491

RESULT 15
Q96372 PRELIMINARY; PRT; 639 AA.
AC Q96372;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE STE20 serine/threonine protein kinase homolog.
GN MBT OR CG18582.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP SEQUENCE FROM N.A.
RA Melnick M.B.;
RT "New Drosophila member of the Ste20 serine/threonine kinase family.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF031517; AAD01935.1; -.
DR HSSP; P24941; 1BUH.
DR FlyBase; FBgn0025743; mbt.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000095; PAKbox/Rhobndng.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00786; PBD; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 639 AA; 69653 MW; 414D2177224C43C6 CRC64;

Query Match 81.0%; Score 366; DB 5; Length 639;
Best Local Similarity 78.7%; Pred. No. 2.4e-34;
Matches 70; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVVMYNSYLVGDELWVMVEFEGGALTDIVTHTRNNEE 60
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Db 403 KQORELLFNEVWIRNDRYHHPNIVETYSFLVNDLWVMEYLEGGALTDIVTHSRMDEE 462  
QY 61 QIAAYCLAVLQALAVLHAGQVHSDIKTD 89  
Db 463 QIATVCKOCLKALAYLHSGQVHHRDIKSD 491

Search completed: September 29, 2004, 18:04:41  
Job time : 20.1559 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:36:56 ; Search time 23.2971 Seconds  
(without alignments)  
1079.395 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_29Jan04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	100.0	89	3 AAY59139	Aay59139 Mouse ser
2	436	96.5	240	4 AAM93297	Aam93297 Human pol
3	436	96.5	240	7 ADC37303	Adc37303 Nuclear f
4	436	96.5	250	3 AAY59129	Aay59129 Human PAK
5	436	96.5	293	7 ADEL5851	Adel5851 PAK4KD pr
6	436	96.5	398	2 AAY55941	Aay55941 Human PAK
7	436	96.5	438	7 ADC37305	Adc37305 Nuclear f
8	436	96.5	501	7 ADC37309	Adc37309 Nuclear f
9	436	96.5	591	3 AAY55964	Aay55964 Full leng
10	436	96.5	591	2 AAY59128	Aay59128 Human ser
11	436	96.5	591	7 ADC37307	Adc37307 Nuclear f
12	436	96.5	591	7 ADD89973	Add89973 Human can
13	436	96.5	620	4 ABG19308	Abg19308 Novel hum
14	407	90.0	547	4 AAG67825	Aag67825 Human pol
15	407	90.0	719	4 AAM38963	Aam38963 Human pol
16	402	88.9	632	4 AAB85788	Aab85788 Human kin
17	402	88.9	719	4 AAB65705	Aab65705 Novel pro
18	402	88.9	719	4 AAE02187	Aae02187 Human p21
19	402	88.9	719	7 ADC37451	Adc37451 Nuclear f
20	379	83.8	311	4 AAB20336	Aab20336 Human PAK
21	379	83.8	641	5 AAE16269	Aae16269 Human kin
22	379	83.8	681	2 AAY55940	Aay55940 Human PAK
23	379	83.8	681	3 AAB03967	Aab03967 Signal tr
24	379	83.8	681	3 AAB03970	Aab03970 Mutant si
25	379	83.8	681	3 AAB03971	Aab03971 Mutant si

## ALIGNMENTS

RESULT 1

AAY59139  
ID AAY59139 standard; protein; 89 AA.

XX  
AC AAY59139;

DT 08-MAR-2000 (first entry)

DE Mouse serine/threonine kinase, PAK4 partial protein sequence.

XX

PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac; Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; mouse; actin polymerization; filopodia; cancer; arthritis.

OS Mus sp.

XX W09963073-A1.

XX 09-DEC-1999.

PF 21-MAY-1999; 99WO-US011341.

XX 21-MAY-1998; 98US-00082737.

PR (UYCO ) UNIV COLUMBIA NEW YORK.

PI Minden A;

DR WPI; 2000-072881/06.

XX N-PSDB; AA240658.

PT Novel mammalian nucleic acid useful for treating cancer and arthritis.

PS Disclosure; Page 44; 95pp; English.

XX The invention relates to an isolated mammalian nucleic acid that encodes PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an effector for the GTPases Rac and Cdc42Hs which are involved in intracellular signal cascades, morphogenesis and mitogenesis, and activate the JNK and p38 MAP kinase pathways. Inhibition of actin polymerization and formation of filopodia. The PAK4 nucleic acid used for recombinant production of the protein, and as a source of probes for identifying homologous sequences and of (anti)sense oligonucleotides for inhibiting PAK4 expression. The protein, or its fragments, are used to raise specific antibodies and these are useful as ligands for therapeutic inhibition of interaction between PAK4 and its native binding partners. Inhibition of PAK4 activity or expression is used for treatment of cancer

CC and arthritis. The present sequence represents the partial sequence of  
CC mouse PAK4  
XX  
SQ Sequence 89 AA;

Query Match 100.0%; Score 452; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1e-50;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89  
DB 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89

RESULT 2  
ID AAM93297 standard; protein; 240 AA.  
XX  
AC AAM93297;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human polypeptide, SEQ ID NO: 2793.  
XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
XX  
OS Homo sapiens.  
XX  
PN EP1130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114089.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
XX  
PR 11-JAN-2000; 2000JP-00118774.  
XX  
PR 02-MAY-2000; 2000JP-00183765.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
DR WPI; 2001-524255/58.  
XX  
DR N-PSDB; AAK94217.  
XX  
PT 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX  
PS Claim 8; SEQ ID NO 2793; 1380pp + Sequence Listing; English.  
XX  
CC The invention relates to primers for synthesising full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesising the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a polypeptide encoded by a full length  
CC human cDNA of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in CD-ROM  
CC format directly from EPO

XX  
SQ Sequence 240 AA;

Query Match 96.5%; Score 436; DB 4; Length 240;  
Best Local Similarity 95.5%; Pred. No. 5e-48;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 5 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 64

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89  
DB 65 QIAAVCLAVLQALAVLHAQGVHSIDIKSD 93

RESULT 3  
ID ADC37303 standard; protein; 240 AA.  
XX  
AC ADC37303;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 136.  
XX  
KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;  
KW cancer; infectious disease; bone disease; AIDS;  
KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;  
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;  
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003048202-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 03-DEC-2002; 2002WO-JP012644.  
XX  
PR 03-DEC-2001; 2001JP-00368692.  
XX  
PR 05-DEC-2001; 2001US-0335829P.  
XX  
PR 03-OCT-2002; 2002JP-00291302.  
XX  
PR 04-OCT-2002; 2002US-0415769P.  
XX  
PA (ASAH ) ASahi KASEI KK.  
XX  
PI Matsuda A, Muramatsu S;  
XX  
DR WPI; 2003-505282/47.  
XX  
DR N-PSDB; ADC37302.  
XX  
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),  
PT useful for treating inflammation, autoimmune diseases, cancers,  
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or  
PT ischemic disorders.  
XX  
PS Claim 1; SEQ ID NO 136; 938pp; English.  
XX  
CC The present invention relates to novel proteins and their coding  
CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-  
CC kappaB). The proteins and their coding sequences are useful for treating  
CC a disease associated with NF-kappaB activation, such as inflammation,  
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,  
CC neurodegenerative diseases, or ischaemic disorders.  
XX  
SQ Sequence 240 AA;

Query Match 96.5%; Score 436; DB 7; Length 240;  
Best Local Similarity 95.5%; Pred. No. 5e-48;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 5 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 64

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89  
DB 65 QIAAVCLAVLQALAVLHAQGVHSIDIKSD 93

```

RESULT 4
AAY59129
ID AAY59129 standard; protein; 250 AA.
XX
AC AAY59129;
XX
DT 08-MAR-2000 (first entry)
XX
DE Human PAK4 kinase domain fragment.
XX
KW PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;
KW Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human;
KW actin polymerization; filopodia; cancer; arthritis; kinase domain.
XX
OS Homo sapiens.
XX
PN WO9963073-A1.
XX
PD 09-DEC-1999.
XX
PF 21-MAY-1999; 99WO-US011341.
XX
PR 21-MAY-1998; 98US-00082737.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Minden A;
XX
DR WPI; 2000-072881/06.
XX
PT Novel mammalian nucleic acid useful for treating cancer and arthritis.
XX
PS Disclosure; Fig 1C; 95pp; English.
XX
CC The invention relates to an isolated mammalian nucleic acid that encodes
CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an
CC effector for the GTPases Rac and Cdc42Hs which are involved in
CC intracellular signal cascades, morphogenesis and mitogenesis, and
CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of
CC PAK4 with these enzymes will thus result in inhibition of actin
CC polymerization and formation of filopodia. The PAK4 nucleic acid used for
CC recombinant production of the protein, and as a source of probes for
CC identifying homologous sequences and of (anti)sense oligonucleotides for
CC inhibiting PAK4 expression. The protein, or its fragments, are used to
CC raise specific antibodies and these are useful as ligands for therapeutic
CC inhibition of interaction between PAK4 and its native binding partners.
CC Inhibition of PAK4 activity or expression is used for treatment of cancer
CC and arthritis. The present sequence represents the kinase domain fragment
CC of human serine/threonine kinase, PAK4
XX
SQ Sequence 250 AA;
Query Match 96.5%; Score 436; DB 3; Length 250;
Best Local Similarity 95.5%; Pred. No. 5.3e-48;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KQORRELFNEVIMRDYQHENVVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 33 KQORRELFNEVIMRDYQHENVVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 92
QY 61 QTAAVCLAVLQALAVTHAQGVTHSDIKTD 89
Db 93 QTAAVCLAVLQALSVLHAQGVTHRDIKSD 121
RESULT 5
ADE15851
ID ADE15851 standard; protein; 293 AA.
XX
AC ADE15851;
XX

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DT 29-JAN-2004 (first entry)
XX
DE PAK4KD protein.
XX
KW PAK4KD protein.
XX
OS Homo sapiens.
XX
PN WO2003087816-A1.
XX
PD 23-OCT-2003.
XX
PF 08-APR-2003; 2003WO-US010878.
XX
PR 09-APR-2002; 2002US-0371018P.
PR 02-DEC-2002; 2002US-0430567P.
XX
PA (STRU-) STRUCTURAL GENOMIX INC.
XX
PI Antonyasamy SS, Feil I, Buchanan SG, Post KW, Liu Y, Lorber D;
XX
DR WPI; 2003-853974/79.
XX
PT Producing a computer-readable database comprising the three-dimensional
PT molecular structural coordinates of a binding pocket of a PAK4KD protein,
PT comprises introducing the structural coordinates into a computer.
XX
PS Claim 17; SEQ ID NO 5; 421pp; English.
XX
CC The present invention relates to producing a computer-readable database
CC comprising the three-dimensional molecular structural coordinates of a
CC binding pocket of a PAK4KD protein, comprising introducing the structural
CC coordinates to into a computer to produce a database containing the
CC molecular structural coordinates of the protein or binding pocket. The
CC method is useful for producing a machine-readable database for
CC identifying and designing inhibitors, activators and mutants of PAK4KD,
CC PAK4KD crystals and compounds or compositions that affect PAK4KD
CC activity. The present sequence represents a primer of the invention.
XX
SQ Sequence 293 AA;
Query Match 96.5%; Score 436; DB 7; Length 293;
Best Local Similarity 95.5%; Pred. No. 6.6e-48;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KQORRELFNEVIMRDYQHENVVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 58 KQORRELFNEVIMRDYQHENVVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 117
QY 61 QTAAVCLAVLQALAVTHAQGVTHSDIKTD 89
Db 118 QTAAVCLAVLQALSVLHAQGVTHRDIKSD 146
RESULT 6
AAY55941
ID AAY55941 standard; protein; 398 AA.
XX
AC AAY55941;
XX
DT 18-FEB-2000 (first entry)
XX
DE Human PAK5 protein.
XX
KW Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;
KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW vulnery; STE20; protein kinase; STIK2; STIK3; STIK4; STIK5; STIK6; STIK7;
KW ZC1; ZC2; ZC3; ZC4; KHS2; SUL01; SUL03; GEK2; PAK4; PAK5; antagonist;
KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW myocardial infarction; cardiovascular disease; stroke; renal failure;

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KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
 KW mesangial disorder; growth regulation; wound healing; T cell activation;  
 KW immunosuppressant.

OS Homo sapiens.  
 XX  
 XX WO9953036-A2.  
 XX  
 XX 21-OCT-1999.  
 XX  
 XX 13-APR-1999; 99WO-US008150.  
 XX  
 XX 14-APR-1999; 98US-0081784F.  
 XX  
 XX (SUGEN-) SUGEN INC.  
 XX  
 XX Plowman G, Martinez R, Whyte D;  
 PI  
 XX WPI; 1999-611301/52.  
 DR  
 DR N-PSDB; AA240493.  
 XX

PT Novel kinase-related polypeptides used for the diagnosis and treatment of  
 PT Kinase-related diseases and disorders.

XX  
 XX Disclosure; Page 310-312; 387pp; English.  
 XX  
 CC This sequence represents a novel STE20-related protein kinase. The  
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide  
 CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,  
 CC ZC4, KHS2, SUJ1, SUJ3, GEK2, PAK4 and PAK5. The proteins are used to  
 CC identify agonists and antagonists, and to raise antibodies. The  
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,  
 CC polypeptides, antibodies, antagonists and agonists may be used to treat  
 CC diseases such as immune-related disorders and diseases (e.g. rheumatoid  
 CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.  
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,  
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory  
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial  
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative  
 CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral  
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,  
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes  
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be  
 CC useful for cell growth regulation (e.g. in wound healing), T cell  
 CC activation, mitosis control, and as immunosuppressants

XX Sequence 398 AA;

Query Match 96.5%; Score 436; DB 2; Length 398;  
 Best Local Similarity 95.5%; Pred. No. 1e-47;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYNSYLGDELWVMEFEGGALTDIVTHRMNEE 60  
 DB 163 KQORRELLFNEVIMRDYRHENVVMYNSYLGDELWVMEFEGGALTDIVTHRMNEE 222

QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89  
 DB 223 QIAAVCLAVLQALVLAHQGVTHSDIKTD 251

RESULT 7  
 ADC37305  
 ID ADC37305 standard; protein; 438 AA.

XX ADC37305;

XX 18-DEC-2003 (first entry)

DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 138.

XX

KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;  
 KW cancer; infectious disease; bone disease; AIDS;  
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;  
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-Hiv;  
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.

OS Homo sapiens.  
 XX  
 XX WO2003048202-A2.  
 XX  
 XX 12-JUN-2003.  
 XX  
 XX 03-DEC-2002; 2002WO-JP012644.  
 XX  
 XX 03-DEC-2001; 2001JP-00368692.  
 XX  
 XX 05-DEC-2001; 2001US-0335829F.  
 PR  
 PR 03-OCT-2002; 2002JP-00291302.  
 PR  
 PR 04-OCT-2002; 2002US-0415769F.  
 XX  
 XX (ASAH ) ASAH KASEI KK.  
 PA  
 XX Matsuda A, Muramatsu S;  
 XX  
 XX WPI; 2003-505282/47.  
 DR  
 DR N-PSDB; ADC37304.

XX New purified protein that activates nuclear factor kappa B (NF-kappaB),  
 PT useful for treating inflammation, autoimmune diseases, cancers,  
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or  
 PT ischemic disorders.

PS Claim 1; SEQ ID NO 138; 938pp; English.

CC The present invention relates to novel proteins and their coding  
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-  
 CC kappaB). The proteins and their coding sequences are useful for treating  
 CC a disease associated with NF-kappaB activation, such as inflammation,  
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,  
 CC neurodegenerative diseases, or ischaemic disorders.

XX Sequence 438 AA;

Query Match 96.5%; Score 436; DB 7; Length 438;  
 Best Local Similarity 95.5%; Pred. No. 1.2e-47;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYNSYLGDELWVMEFEGGALTDIVTHRMNEE 60  
 DB 203 KQORRELLFNEVIMRDYRHENVVMYNSYLGDELWVMEFEGGALTDIVTHRMNEE 262

QY 61 QIAAVCLAVLQALVLAHQGVTHSDIKTD 89  
 DB 263 QIAAVCLAVLQALVLAHQGVTHSDIKTD 291

RESULT 8  
 ADC37309  
 ID ADC37309 standard; protein; 501 AA.

XX ADC37309;

XX 18-DEC-2003 (first entry)

XX Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 142.

XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;  
 KW cancer; infectious disease; bone disease; AIDS;  
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;  
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-Hiv;  
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.

OS Homo sapiens.

XX





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XX 09-DEC-1999.
XX 21-MAY-1999; 99WO-US011341.
XX 21-MAY-1999; 98US-00082737.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX Minden A;
XX WPI; 2000-072881/06.
XX N-PSDB; AA240657.
XX Novel mammalian nucleic acid useful for treating cancer and arthritis.
XX Claim 8; Fig 1A-B; 95pp; English.
XX The invention relates to an isolated mammalian nucleic acid that encodes
CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an
CC effector for the GTPases Rac and Cdc42Hs which are involved in
CC intracellular signal cascades, morphogenesis and mitogenesis, and
CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of
CC PAK4 with these enzymes will thus result in inhibition of actin
CC polymerization and formation of filopodia. The PAK4 nucleic acid used for
CC recombinant production of the protein, and as a source of probes for
CC identifying homologous sequences and of (anti)sense oligonucleotides for
CC inhibiting PAK4 expression. The protein, or its fragments, are used to
CC raise specific antibodies and these are useful as ligands for therapeutic
CC inhibition of interaction between PAK4 and its native binding partners.
CC Inhibition of PAK4 activity or expression is used for treatment of cancer
CC and arthritis. The present sequence represents the human serine/threonine
CC kinase, PAK4
XX
XX Sequence 591 AA;
SQ
Query Match 96.5%; Score 436; DB 3; Length 591;
Best Local Similarity 95.5%; Pred. No. 1.8e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KOORRELLFNEVIMRDYRHENVVEMVNSYLVGDELWVWMEFEGGALTDIVTHTRMNEE 60
DB 356 KOORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVWMEFEGGALTDIVTHTRMNEE 415
QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
DB 416 QIAAVCLAVLQALSVLHAQGVHRIKSD 444
RESULT 11
ID ADC37307
XX ADC37307 standard; protein; 591 AA.
XX ADC37307;
XX 18-DEC-2003 (first entry)
XX Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 140.
XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
XX cancer; infectious disease; bone disease; AIDS;
XX neurodegenerative disease; ischaemic disorder; Antiinflammatory;
XX Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
XX Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
XX Homo sapiens.
XX WO2003048202-A2.
XX 12-JUN-2003.
XX 03-DEC-2002; 2002WO-JP012644.
XX

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PR 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX (ASAH ) ASahi KASEI KK.
XX Matsuda A, Muramatsu S;
XX WPI; 2003-505282/47.
XX N-PSDB; ADC37306.
XX New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX Claim 1; SEQ ID NO 140; 938pp; English.
XX The present invention relates to novel proteins and their coding
CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischaemic disorders.
XX Sequence 591 AA;
SQ
Query Match 96.5%; Score 436; DB 7; Length 591;
Best Local Similarity 95.5%; Pred. No. 1.8e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KOORRELLFNEVIMRDYRHENVVEMVNSYLVGDELWVWMEFEGGALTDIVTHTRMNEE 60
DB 356 KOORRELLFNEVIMRDYQHENVVEMVNSYLVGDELWVWMEFEGGALTDIVTHTRMNEE 415
QY 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
DB 416 QIAAVCLAVLQALSVLHAQGVHRIKSD 444
RESULT 12
ID ADD89973
XX ADD89973 standard; protein; 591 AA.
XX AC ADD89973;
XX 29-JAN-2004 (first entry)
XX Human cancer-associated protein kinase PAK4.
XX PAK4; protein kinase; enzyme; cancer; cytostatic; immunosuppressive;
XX antidiabetic; antirheumatic; antiarthritic; antipsoriatic;
XX antiangiogenic; antiarteriosclerotic; antiinflammatory; vulnerary;
XX gynaecological; neuroprotective; gene therapy; human.
XX Homo sapiens.
XX WO2003083096-A2.
XX 09-OCT-2003.
XX 21-MAR-2003; 2003WO-CA000409.
XX 28-MAR-2002; 2002US-0368853P.
XX (KINE-) KINETEK PHARM INC.
XX Delaney AD;
XX WPI; 2003-833542/77.
XX N-PSDB; ADD89972.
XX

```

PT New nucleic acids encoding cancer associated protein kinases, useful as  
PT targets for screening pharmaceutical agents that inhibit the growth of  
PT tumor cells, or for diagnosing and treating cancer, inflammation or  
PT autoimmune disease.

XX Claim 1; Page 77-78; 91pp; English.

XX The present sequence is the protein sequence of human cancer-associated  
CC protein kinase, PAK4. PAK-related kinase PAK4 is an effector molecule for  
CC Cdc42Hs. Its gene expression is up-regulated in cancers of the brain,  
CC lung, muscle and uterus. PAK4 is one of a set of protein kinases that are  
CC shown by the invention to be over-expressed in hyper-proliferative cells.  
CC These protein kinases provide targets for drug screening for agents  
CC effective in inhibiting the growth or metastasis of tumour cells, and for  
CC determining other molecular targets in kinase signal transduction  
CC pathways involved in transformation and growth of tumour cells. A claimed  
CC method for inhibiting the growth of a cancer cell involves down-  
CC regulating the activity of the protein kinase using an antisense sequence  
CC or inhibitor of kinase activity, especially where the cancer cell is a  
CC breast, liver, colon, muscle, prostate, kidney, lung, placental or  
CC uterine cancer cell. Detection of over-expression in cancers provides a  
CC useful diagnostic for predicting patient prognosis and probability of  
CC drug effectiveness. Agents that specifically bind the protein kinases can  
CC be used for treatment and visualisation of tumours in patients. The  
CC protein kinase polypeptides and nucleic acids may also be used for  
CC treating hyperproliferative diseases, such as autoimmune disease,  
CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis,  
CC atherosclerosis, inflammation, scarring, endometriosis and angiogenesis.

XX Sequence 591 AA;

Query Match 96.5%; Score 436; DB 7; Length 591;  
Best Local Similarity 95.5%; Pred. No. 1.8e-47;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60  
DB 356 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 415  
QY 61 QIAAVCLAVLQALSVLHAQGVVHSDIKTD 89  
DB 416 QIAAVCLAVLQALSVLHAQGVVHSDIKSD 444

RESULT 13  
ABG19308  
ID ABG19308 standard; protein; 620 AA.

AC ABG19308;  
DT 18-FEB-2002 (first entry)  
XX Novel human diagnostic protein #19299.

DE Human; Chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS83495.

XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX Claim 20; SEQ ID NO 49667; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 620 AA;

Query Match 96.5%; Score 436; DB 4; Length 620;  
Best Local Similarity 95.5%; Pred. No. 1.9e-47;  
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60  
DB 385 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELWVMEFEGGALTDIVTHTRMNEE 444  
QY 61 QIAAVCLAVLQALSVLHAQGVVHSDIKTD 89  
DB 445 QIAAVCLAVLQALSVLHAQGVVHSDIKSD 473

RESULT 14  
AAG67825  
ID AAG67825 standard; protein; 547 AA.

XX AAG67825;

XX 26-OCT-2001 (first entry)

XX Human P21-active kinase 60 protein.

XX Human; P21-active kinase 60; malignant tumour; nosohemia; HIV infection;  
KW immunological disease; inflammation.

XX Homo sapiens.

XX CN1298009-A.

XX 06-JUN-2001.

XX 29-NOV-1999; 99CN-00124147.

XX 29-NOV-1999; 99CN-00124147.

XX (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.

XX Mao Y, Xie Y, Gu Y;

DR WPI; 2001-489684/54.  
DR N-PSDB; AAH44557.  
XX  
PT Human P21-active kinase 60 as one new kind of polypeptide and  
XX polynucleotides encoding this polypeptide.  
XX  
PS Claim 1; Page 25-26 (Disclosure); 33pp; Chinese.  
XX  
CC The present sequence represents human P21-active kinase 60. The present  
CC invention also describes a method of applying the polypeptide in treating  
CC various diseases, such as malignant tumour, nosohemia, HIV infection,  
CC immunological diseases and inflammations. Also described is an antagonist  
CC resisting the polypeptide and its treatment effect  
XX  
SQ Sequence 547 AA;  
Query Match 90.0%; Score 407; DB 4; Length 547;  
Best Local Similarity 87.6%; Pred. No. 9.3e-44;  
Matches 78; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 312 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 371  
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89  
DB 372 QIATVCLSVLRALSYLHNQGVHRIKSD 400  
RESULT 15  
ID AAM38963 standard; protein; 719 AA.  
AC AAM38963;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2108.  
XX  
KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
XX WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR N-PSDB; AAI58119.  
XX

PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 3; SEQ ID NO 2108; 10078pp; English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with nontropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 719 AA;  
Query Match 90.0%; Score 407; DB 4; Length 719;  
Best Local Similarity 87.6%; Pred. No. 1.4e-43;  
Matches 78; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
QY 1 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60  
DB 484 KQORRELLFNEVIMRDYRHENNVEMVNSYLVGDELWVMEFEGGALTDIVTHRMNEE 543  
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89  
DB 544 QIATVCLSVLRALSYLHNQGVHRIKSD 572  
Search completed: September 29, 2004, 18:01:39  
Job time : 24.2971 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:01:47 ; Search time 22.25 Seconds  
(without alignments)  
1287.197 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	100.0	89	16	US-10-693-367-14
2	443	98.0	292	15	US-10-406-676-7
3	443	98.0	292	15	US-10-406-676-7
4	436	96.5	250	16	US-10-693-367-3
5	436	96.5	292	15	US-10-406-676-5
6	436	96.5	292	15	US-10-406-676-6
7	436	96.5	292	15	US-10-406-676-8
8	436	96.5	292	15	US-10-406-676-9
9	436	96.5	292	15	US-10-406-676-10
10	436	96.5	292	15	US-10-406-676-11
11	436	96.5	293	15	US-10-406-676-4
12	436	96.5	398	10	US-09-291-417-30
13	436	96.5	588	14	US-10-134-102-1
14	436	96.5	591	10	US-09-291-417-103
15	436	96.5	591	14	US-10-134-102-4

16	436	96.5	591	15	US-10-394-322A-48	Sequence 48, Appl
17	436	96.5	591	16	US-10-693-367-2	Sequence 2, Appl
18	421	93.1	292	15	US-10-406-676-15	Sequence 15, Appl
19	407	90.0	290	15	US-10-406-676-13	Sequence 13, Appl
20	407	90.0	719	14	US-10-331-095-2	Sequence 2, Appl
21	402	88.9	290	15	US-10-406-676-14	Sequence 14, Appl
22	402	88.9	290	15	US-10-406-676-16	Sequence 16, Appl
23	402	88.9	290	15	US-10-406-676-17	Sequence 17, Appl
24	402	88.9	580	15	US-10-108-260A-3288	Sequence 3288, Ap
25	402	88.9	719	14	US-10-331-095-4	Sequence 4, Appl
26	402	88.9	719	15	US-10-394-322A-49	Sequence 49, Appl
27	379	83.8	292	15	US-10-406-676-21	Sequence 21, Appl
28	379	83.8	641	16	US-10-311-034-15	Sequence 15, Appl
29	379	83.8	681	10	US-09-291-417-29	Sequence 29, Appl
30	376	83.2	681	10	US-09-765-815-2	Sequence 2, Appl
31	366	81.0	290	15	US-10-406-676-18	Sequence 18, Appl
32	366	81.0	290	15	US-10-406-676-19	Sequence 19, Appl
33	366	81.0	290	15	US-10-406-676-20	Sequence 20, Appl
34	366	81.0	635	14	US-10-134-102-2	Sequence 2, Appl
35	366	81.0	639	14	US-10-134-102-6	Sequence 6, Appl
36	303	67.0	540	15	US-10-369-493-6482	Sequence 6482, Ap
37	303	67.0	542	15	US-10-369-493-6483	Sequence 6483, Ap
38	283	62.6	704	12	US-10-267-502-378	Sequence 378, App
39	277	61.3	297	16	US-10-664-421-34	Sequence 34, Appl
40	277	61.3	305	10	US-09-765-815-10	Sequence 10, Appl
41	277	61.3	326	16	US-10-664-421-48	Sequence 48, Appl
42	277	61.3	545	9	US-09-967-624-5	Sequence 5, Appl
43	277	61.3	545	12	US-10-262-511-30	Sequence 30, Appl
44	277	61.3	545	12	US-10-267-502-380	Sequence 380, App
45	277	61.3	545	12	US-10-267-502-383	Sequence 383, App

## ALIGNMENTS

### RESULT 1

US-10-693-367-14  
; Sequence 14, Application US/10693367  
; Publication No. US20040091992A1  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE  
; FILE REFERENCE: 575/55311-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/693,367  
; CURRENT FILING DATE: 2003-10-24  
; PRIOR APPLICATION NUMBER: US/09/718,032  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: PCT/US99/11341  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 09/082,737  
; PRIOR FILING DATE: 1998-05-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 14  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: mouse  
; US-10-693-367-14

Query Match 100.0%; Score 452; DB 16; Length 89;  
Best Local Similarity 100.0%; Pred. No. 7,9e-45;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KQORRELFNEVIMRDYRHENNVNYSYLVGDELWVMEFEGGALTDIVHTHTRNEE	60
Db	1	KQORRELFNEVIMRDYRHENNVNYSYLVGDELWVMEFEGGALTDIVHTHTRNEE	60
Qy	61	QIAAVCLAVLQALAVLHAQGVHSDIKTD	89
Db	61	QIAAVCLAVLQALAVLHAQGVHSDIKTD	89



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; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-5

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELFNEVVIMRDYHENVNVMYNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEE 60
DB 57 KQORRELFNEVVIMRDYHENVNVMYNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEE 116
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 117 QIAAVCLAVLQALSVLHAQGVHSDIKSD 145

RESULT 6
US-10-406-676-6
; Sequence 6, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-6

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELFNEVVIMRDYHENVNVMYNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEE 60
DB 57 KQORRELFNEVVIMRDYHENVNVMYNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEE 116
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 117 QIAAVCLAVLQALSVLHAQGVHSDIKSD 145

RESULT 7
US-10-406-676-8
; Sequence 8, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
```

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; TITLE OF INVENTION: PAK4KD
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-8

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELFNEVVIMRDYHENVNVMYNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEE 60
DB 57 KQORRELFNEVVIMRDYHENVNVMYNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEE 116
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 117 QIAAVCLAVLQALSVLHAQGVHSDIKSD 145

RESULT 8
US-10-406-676-9
; Sequence 9, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-9

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELFNEVVIMRDYHENVNVMYNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEE 60
DB 57 KQORRELFNEVVIMRDYHENVNVMYNSYLVGDELWVWMEFLEGGALTDIVTHTRMNEE 116
QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 117 QIAAVCLAVLQALSVLHAQGVHSDIKSD 145

RESULT 9
US-10-406-676-10
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```

; Sequence 10, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-10

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYNYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 57 KQORRELLFNEVIMRDYQHENVVEMYNYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 116

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 117 QIAAVCLAVLQALSVLHAQGVHSDIKSD 145

RESULT 11
US-10-406-676-4
; Sequence 4, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-4

Query Match          96.5%; Score 436; DB 15; Length 293;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYNYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 58 KQORRELLFNEVIMRDYQHENVVEMYNYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 117

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 118 QIAAVCLAVLQALSVLHAQGVHSDIKSD 146

RESULT 12
US-09-291-417-30
; Sequence 30, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mammalian (Human) PAK5
US-09-291-417-30

; Sequence 10, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-11

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYNYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 57 KQORRELLFNEVIMRDYQHENVVEMYNYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 116

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
Db 117 QIAAVCLAVLQALSVLHAQGVHSDIKSD 145

RESULT 10
US-10-406-676-11
; Sequence 11, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-11

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.5e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Query Match          96.5%; Score 436; DB 10; Length 398;
Best Local Similarity 95.5%; Pred. No. 3.6e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 163 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 222

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 223 QIAAVCLAVLQALAVLHAQGVHSDIKTD 251

RESULT 13
US-10-134-102-1
; Sequence 1, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Melnick, Michael B.
; APPLICANT: Moritz, Albrecht
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/173,939
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-1

Query Match          96.5%; Score 436; DB 14; Length 588;
Best Local Similarity 95.5%; Pred. No. 5.8e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 416 QIAAVCLAVLQALAVLHAQGVHSDIKTD 444

RESULT 14
US-09-291-417-103
; Sequence 103, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Full Length Mammalian (Human) PAK5hu
US-09-291-417-103
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Query Match          96.5%; Score 436; DB 10; Length 591;
Best Local Similarity 95.5%; Pred. No. 5.9e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 416 QIAAVCLAVLQALAVLHAQGVHSDIKTD 444

RESULT 15
US-10-134-102-4
; Sequence 4, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Melnick, Michael B.
; APPLICANT: Moritz, Albrecht
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/173,939
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-4

Query Match          96.5%; Score 436; DB 14; Length 591;
Best Local Similarity 95.5%; Pred. No. 5.9e-42;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 KQORRELLFNEVVIMRDYQHENVNVMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 416 QIAAVCLAVLQALAVLHAQGVHSDIKTD 444

Search completed: September 29, 2004, 18:09:25
Job time : 22.25 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:58:42 ; Search time 6.15147 Seconds  
(without alignments)  
746.929 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLHAQGVHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2.6/prodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2.6/prodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2.6/prodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2.6/prodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2.6/prodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2.6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	452	100.0	89	4	US-09-718-032-14
2	436	96.5	250	3	US-09-082-737-3
3	436	96.5	250	4	US-09-718-032-3
4	436	96.5	398	4	US-09-688-188B-30
5	436	96.5	398	4	US-09-291-417D-30
6	436	96.5	591	3	US-09-082-737-2
7	436	96.5	591	4	US-09-688-188B-103
8	436	96.5	591	4	US-09-718-032-2
9	436	96.5	591	4	US-09-291-417D-103
10	379	83.8	681	4	US-09-688-188B-29
11	379	83.8	681	4	US-09-291-417D-29
12	376	83.2	681	4	US-09-765-815-2
13	277	61.3	244	4	US-09-163-507-2
14	277	61.3	268	3	US-08-852-743-3
15	277	61.3	268	3	US-09-185-370-3
16	277	61.3	305	4	US-09-765-815-10
17	277	61.3	465	2	US-08-114-555A-2
18	277	61.3	465	3	US-08-559-397A-2
19	276	61.1	245	4	US-09-163-507-3
20	276	61.1	545	2	US-08-935-760-4
21	276	61.1	545	4	US-09-688-188B-93
22	276	61.1	545	4	US-09-291-417D-93
23	274	60.6	244	4	US-09-163-507-1
24	274	60.6	524	2	US-08-615-942A-2
25	274	60.6	524	4	US-09-237-325-2
26	274	60.6	544	2	US-08-935-760-2
27	274	60.6	544	3	US-08-559-397A-19

28	269	59.5	544	4	US-09-688-188B-95	Sequence 95, Appl
29	269	59.5	544	4	US-09-291-417D-95	Sequence 95, Appl
30	268	59.3	544	3	US-08-559-397A-30	Sequence 30, Appl
31	266	58.8	250	4	US-09-718-032-4	Sequence 4, Appl
32	266	58.8	506	1	US-08-369-780-2	Sequence 2, Appl
33	266	58.8	506	1	US-08-475-682-2	Sequence 2, Appl
34	266	58.8	506	1	US-08-780-833-2	Sequence 2, Appl
35	266	58.8	506	1	US-08-636-036-2	Sequence 2, Appl
36	266	58.8	506	3	US-08-918-509-2	Sequence 2, Appl
37	266	58.8	506	3	US-09-108-262-2	Sequence 2, Appl
38	266	58.8	506	4	US-09-688-188B-94	Sequence 94, Appl
39	266	58.8	506	4	US-09-291-417D-94	Sequence 94, Appl
40	255	56.4	250	4	US-09-718-032-5	Sequence 5, Appl
41	255	56.4	251	3	US-09-082-737-5	Sequence 5, Appl
42	255	56.4	271	2	US-08-852-743-4	Sequence 4, Appl
43	255	56.4	271	3	US-09-185-370-4	Sequence 31, Appl
44	255	56.4	694	3	US-08-559-397A-31	Sequence 29, Appl
45	249	55.1	544	3	US-08-559-397A-29	

## ALIGNMENTS

RESULT 1  
US-09-718-032-14  
; Sequence 14, Application US/09718032  
; Patent No. 6667168  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE  
; FILE REFERENCE: 575/55311-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/718,032  
; CURRENT FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: PCT/US99/11341  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 09/082,737  
; PRIOR FILING DATE: 1998-05-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-718-032-14

Query Match 100.0%; Score 452; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.6e-50;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVHTRMNEE	60
Db	1	KQORRELFNEVIMRDYRHENVMYNSYLVGDELWVMEFEGGALTDIVHTRMNEE	60

RESULT 2  
US-09-082-737-3  
; Sequence 3, Application US/09082737  
; Patent No. 6013500  
; GENERAL INFORMATION:  
; APPLICANT: Minden, Audrey  
; TITLE OF INVENTION: PAK4; A No. 6013500a1 Gene Encoding A Serine/  
; TITLE OF INVENTION: Threonine Kinase  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York

```

RESULT 3
US-09-718-032-3
; Sequence 3, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Manden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: human
US-09-718-032-3

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	Query Match	96.5%	Score 436;	DB 4;	Length 250;
	Best Local Similarity	95.5%;	Pred. No. 7.6e-48;		
	Matches	85;	Conservative	3;	Mismatches 1;
					Indels 0;
					Gaps 0;
Qy	1	KQQRRELLFNENVIMRDYRHENVVEMYSYLVGDELWVMVEFLGGALTDIVVTHRNNEE	60		
Db	33	KQQRRELLFNENVIMRDYQHENVVEMYSYLVGDELWVMVEFLGGALTDIVVTHRNNEE	92		
Qy	61	QIARAVCLAVLQALAVLHAQQGVTHSDIKTD	89		

Query Match	96.5%;	Score 436;	DB 4;	Length 398;
Best Local Similarity	95.5%;	Pred. No. 1.4e-47;		
Matches 8;	Conservative	3;	Mismatches 1;	Indels 0; Gaps 0;
Qy	1	KQORRELFNFVVMIRYHENVEMVNSYLVGDELWVVMFEFEGGALTDIVVTHRMNEE	60	
Db	163	KQORRELFNFVVMIRYQHENVEMVNSYLVGDELWVVMFEFEGGALTDIVVTHRMNEE	222	
Qy	61	QIAAVCLAVLQALAVLHAQGVHSIDKTD	89	
Db	223	QIAAVCLAVLQALSVLHAQGVHRIKSD	251	

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RESULT 5
US-09-291-417D-30
; Sequence 30, Application US/09291417D
; Patent NO. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-30

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Query Match	96.5%	Score 436;	DB 4;	Length 398;
Best Local Similarity	95.5%;	Pred. No. 1.4e-47;		
Matches	85; Conservative	3; Mismatches	1; Indels	0; Gaps 0;
Qy	1	KQQRRELLFNEVIMRDIYRHENVVMYSNLVGDELWWMFEFLGGALTDIVVHTRNNEE	60	
Dd	163	KQQRRELLFNEVIMRDIYQHENVVMYSNLVGDELWWMFEFLGGALTDIVVHTRNNEE	222	
Qy	61	QIAAVCLAVLQAALVLHAQGVIHSIDIKTD	89	
Dd	223	QIAAVCLAVLQAALSVLHAQGVIHRDKSD	251	

RESULT 6  
 US-09-082-737-2  
 ; Sequence 2, Application US/09082737  
 ; Patent No. 6013500  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Minden, Audrey  
 ; TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/  
 ; TITLE OF INVENTION: Threonine Kinase  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 11230  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/082,737  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 0575/55311  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 278-0400  
 ; TELEFAX: (212) 391-0525  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 591 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-082-737-2

Query Match 96.5%; Score 436; DB 3; Length 591;  
 Best Local Similarity 95.5%; Pred. No. 2.5e-47;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KQORRELLFNEVIMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60  
 DB 356 KQORRELLFNEVIMRDYQHENVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415  
 QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89  
 DB 416 QIAAVCLAVLQALSVLHAQGVHSDIKSD 444

RESULT 7  
 US-09-688-188B-103  
 ; Sequence 103, Application US/09688188B  
 ; Patent No. 6656716  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLOWMAN, GREGORY  
 ; APPLICANT: MARTINEZ, RICARDO  
 ; APPLICANT: WHYTE, DAVID  
 ; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
 ; FILE REFERENCE: 038602/0328  
 ; CURRENT APPLICATION NUMBER: US/09/688,188B  
 ; CURRENT FILING DATE: 2000-10-16  
 ; PRIOR APPLICATION NUMBER: 09/291,417  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: 60/081,784  
 ; PRIOR FILING DATE: 1998-04-14  
 ; NUMBER OF SEQ ID NOS: 155  
 ; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 103  
 ; LENGTH: 591  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-688-188B-103  
 Query Match 96.5%; Score 436; DB 4; Length 591;  
 Best Local Similarity 95.5%; Pred. No. 2.5e-47;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KQORRELLFNEVIMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60  
 DB 356 KQORRELLFNEVIMRDYQHENVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415  
 QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89  
 DB 416 QIAAVCLAVLQALSVLHAQGVHSDIKSD 444

RESULT 8  
 US-09-718-032-2  
 ; Sequence 2, Application US/09718032  
 ; Patent No. 6667168  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Trustees of Columbia University  
 ; APPLICANT: Minden, Audrey  
 ; TITLE OF INVENTION: PAK4; A NOVEL GENE ENCODING A SERINE/THREONINE KINASE  
 ; FILE REFERENCE: 575/55311-A-PCT-US  
 ; CURRENT APPLICATION NUMBER: US/09/718,032  
 ; CURRENT FILING DATE: 2000-11-21  
 ; PRIOR APPLICATION NUMBER: PCT/US99/11341  
 ; PRIOR FILING DATE: 1999-05-21  
 ; PRIOR APPLICATION NUMBER: 09/082,737  
 ; PRIOR FILING DATE: 1998-05-21  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 591  
 ; TYPE: PRT  
 ; ORGANISM: human  
 ; US-09-718-032-2

Query Match 96.5%; Score 436; DB 4; Length 591;  
 Best Local Similarity 95.5%; Pred. No. 2.5e-47;  
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KQORRELLFNEVIMRDYRHENNVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 60  
 DB 356 KQORRELLFNEVIMRDYQHENVNMYNSYLVGDELWVVMFELEGALTDIVTHTRMNEE 415  
 QY 61 QIAAVCLAVLQALSVLHAQGVHSDIKTD 89  
 DB 416 QIAAVCLAVLQALSVLHAQGVHSDIKSD 444

RESULT 9  
 US-09-291-417D-103  
 ; Sequence 103, Application US/09291417D  
 ; Patent No. 6680170  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLOWMAN, GREGORY  
 ; APPLICANT: MARTINEZ, RICARDO  
 ; APPLICANT: WHYTE, DAVID  
 ; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
 ; FILE REFERENCE: 038602/0329  
 ; CURRENT APPLICATION NUMBER: US/09/291,417D  
 ; CURRENT FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: 60/081,784  
 ; PRIOR FILING DATE: 1998-04-14  
 ; NUMBER OF SEQ ID NOS: 155  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 103  
 ; LENGTH: 591

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-103

Query Match      96.5%; Score 436; DB 4; Length 591;
Best Local Similarity 95.5%; Pred. No. 2.5e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 356 KQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 415

QY 61 QIAAVCLAVLQALVLAHQAQGVHSDIKTD 89
Db 416 QIAAVCLAVLQALVLAHQAQGVHSDIKSD 444

RESULT 10
US-09-688-188B-29
; Sequence 29, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STB20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-29

Query Match      83.8%; Score 379; DB 4; Length 681;
Best Local Similarity 83.1%; Pred. No. 5.9e-40;
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 442 KQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFEGGALTDIVSQVRLNEE 501

QY 61 QIAAVCLAVLQALVLAHQAQGVHSDIKTD 89
Db 502 QIATVCEAVLQALVLAHQAQGVHSDIKSD 530

RESULT 11
US-09-291-417D-29
; Sequence 29, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STB20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-29

Query Match      83.8%; Score 379; DB 4; Length 681;
Best Local Similarity 83.1%; Pred. No. 5.9e-40;
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 442 KQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFEGGALTDIVSQVRLNEE 501

QY 61 QIAAVCLAVLQALVLAHQAQGVHSDIKTD 89
Db 502 QIATVCEAVLQALVLAHQAQGVHSDIKSD 530

RESULT 12
US-09-765-815-2
; Sequence 2, Application US/09765815
; Patent No. 6673586
; GENERAL INFORMATION:
; APPLICANT: Balk, Steven
; TITLE OF INVENTION: No. 6673586el Steroid Hormone Receptor
; TITLE OF INVENTION: Interacting Protein Kinase
; FILE REFERENCE: 01948/068002
; CURRENT APPLICATION NUMBER: US/09/765,815
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/176,859
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-765-815-2

Query Match      83.2%; Score 376; DB 4; Length 681;
Best Local Similarity 82.0%; Pred. No. 1.4e-39;
Matches 73; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENNVEMYSYLVGDELWVMEFEGGALTDIVTHTRMNEE 60
Db 442 KQORRELLFNEVIMRDYQHENVVEMYSYLVGDELWVMEFEGGALTDIVSQVRLNEE 501

QY 61 QIAAVCLAVLQALVLAHQAQGVHSDIKTD 89
Db 502 QIATVCEAVLQALVLAHQAQGVHSDIKSD 530

RESULT 13
US-09-163-507-2
; Sequence 2, Application US/09163507
; Patent No. 6383734
; GENERAL INFORMATION:
; APPLICANT: Marshall, M. S.
; APPLICANT: Diaz, H. B.
; APPLICANT: King, A. J.
; APPLICANT: Sun, H.
; TITLE OF INVENTION: Method to determine inhibition of PAK3
; TITLE OF INVENTION: activation of RAF-1
; FILE REFERENCE: 740.001US1
; CURRENT APPLICATION NUMBER: US/09/163,507
; CURRENT FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-163-507-2

Query Match      61.3%; Score 277; DB 4; Length 244;
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Blank

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 17:38:51 ; Search time 2.48676 Seconds  
(without alignments)  
1863.563 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452

Sequence: 1 KQORRELLFNEVIMRDYRH.....LQALAVLHAQGVHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	436	96.5	591	1 PAK4 HUMAN	O96013 homo sapien
2	402	88.9	719	1 PAK7 HUMAN	O9p286 homo sapien
3	379	83.8	681	1 PAK6 HUMAN	O9nq05 homo sapien
4	277	61.3	544	1 PAK1 RAT	P35465 rattus norv
5	277	61.3	545	1 PAK1 HUMAN	O13153 homo sapien
6	277	61.3	545	1 PAK1 MOUSE	O88643 mus musculu
7	276	61.1	544	1 PAK3 HUMAN	O75914 homo sapien
8	276	61.1	544	1 PAK3 RAT	O62829 rattus norv
9	274	60.6	524	1 PAK2 HUMAN	O13177 homo sapien
10	274	60.6	524	1 PAK2 RABIT	O29502 oryctolagus
11	274	60.6	524	1 PAK2 RAT	O64303 rattus norv
12	269	59.5	544	1 PAK3 MOUSE	O61036 mus musculu
13	256	56.6	1230	1 ST20 CANAL	O92212 candida alb
14	255	56.4	939	1 ST20 YEAST	O03497 saccharomyc
15	248.5	55.0	971	1 CLA4 CANAL	O14427 candida alb
16	231.5	51.2	842	1 CLA4 YEAST	P48562 saccharomyc
17	231	51.1	658	1 PAK1 SCHPO	P50527 schizosacch
18	220.5	48.8	589	1 SKM1 YEAST	O10056 schizosacch
19	203.5	45.0	655	1 SKM1 YEAST	O61161 mus musculu
20	180.5	39.9	821	1 M4K2 MOUSE	O12851 h mitogen-a
21	177.5	39.3	819	1 M4K2 HUMAN	O99100 mus musculu
22	172.5	38.2	681	1 M4K3 MOUSE	O92412 rattus norv
23	172.5	38.2	862	1 M4K3 RAT	O8i0v8 homo sapien
24	172.5	38.2	894	1 M4K3 HUMAN	O92918 homo sapien
25	170.5	37.7	833	1 M4K1 HUMAN	O8bpm2 mus musculu
26	170.5	37.7	847	1 M4K5 MOUSE	O9y4k4 homo sapien
27	169.5	37.5	846	1 M4K5 HUMAN	P70218 mus musculu
28	164.5	36.4	827	1 M4K1 MOUSE	O9jms2 mus musculu
29	161	35.6	1308	1 M4K6 MOUSE	O8n4c8 homo sapien
30	161	35.6	1332	1 M4K6 HUMAN	O9uew8 homo sapien
31	157.5	34.8	547	1 SPK4 HUMAN	O88506 rattus norv
32	157.5	34.8	553	1 SPK4 RAT	O9z1w9 mus musculu
33	157.5	34.8	556	1 SPK4 MOUSE	

34	157	34.7	916	1 TN1K MOUSE	P83510 mus musculu
35	157	34.7	1360	1 TN1K HUMAN	O9uRe5 homo sapien
36	151.5	33.5	1401	1 WIS4 SCHPO	O14299 schizosacch
37	151	33.4	944	1 NER9 XENLA	O7zzc8 xenopus lae
38	148.5	32.9	652	1 NAK1 SCHPO	O75011 schizosacch
39	146	32.3	1233	1 M4K4 MOUSE	P97820 mus musculu
40	145.5	32.2	1080	1 M115 CAEEL	O23356 caenorhabdi
41	145.5	32.2	1314	1 SS22 YEAST	P25390 saccharomyc
42	145	32.1	471	1 SIDI SCHPO	O14305 schizosacch
43	145	32.1	1239	1 M4K4 HUMAN	O95819 homo sapien
44	141.5	31.3	1050	1 ULK1 HUMAN	O75385 homo sapien
45	141.5	31.3	1051	1 ULK1 MOUSE	O70405 mus musculu

## ALIGNMENTS

RESULT 1  
PAK4\_HUMAN STANDARD; PRT; 591 AA.  
AC O96013; Q9BU33;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.-) (p21-activated kinase 4) (PAK-4).  
GN PAK4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=99043860; PubMed=9822598;  
RA Abo A., Qu J., Cammarano M.S., Dan C., Fritsch A., Baud V., Belisle B., Minden A.;  
RT "PAK4, a novel effector for Cdc42Hs, is implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia";  
RT EMBO J. 17:6527-6540(1998).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX Melnick M.B.;  
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Eye, Pancreas, and Placenta;  
MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: ACTIVATES THE JNK PATHWAY. IMPLICATED IN THE REORGANIZATION OF THE ACTIN CYTOSKELETON AND IN THE FORMATION OF FILOPODIA.  
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND WEAKLY WITH RAC1.  
CC



```

CC      -!- SIMILARITY: Contains 1 CRIB domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB040812; BAA94194.1; -.
DR      EMBL; AB033090; BAA86578.1; ALT INIT.
DR      EMBL; AL353612; CAC34367.1; -.
DR      HSSP; P24941; 1BUH.
DR      Genew; HGNC:15916; PAK7.
DR      MIM; 608038; -.
DR      InterPro; IPR000095; PAKbox/RhoDbndng.
DR      InterPro; IPR000719; Prot Kinase.
DR      InterPro; IPR008271; Ser thr pkin AS.
DR      InterPro; IPR002290; Ser thr pkinase.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF00786; PBD; 1.
DR      Pfam; PF00069; pkinase; 1.
DR      PRINTS; PD00109; TYRKINASE.
DR      ProDom; PD000001; Prot Kinase; 1.
DR      SMART; SM00285; PBD; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS50108; CRIB; 1.
DR      PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE NEG.
KW      Transferase; Serine/threonine-protein kinase; ATP-binding;
KW      Phosphorylation.
FT      DOMAIN 11 24 CRIB.
FT      DOMAIN 25 448 LINKER.
FT      DOMAIN 449 700 PROTEIN KINASE.
FT      NP_BIND 455 463 ATP (BY SIMILARITY).
FT      BINDING 478 478 ATP (BY SIMILARITY).
FT      ACT_SITE 568 568 BY SIMILARITY.
SQ      SEQUENCE 719 AA; 80744 MW; 07A12B1EEC4E2A02 CRC64;

Query Match      88.9%; Score 402; DB 1; Length 719;
Best Local Similarity 86.5%; Pred. No. 1.1e-33;
Matches 77; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 KOORRELLFNEVIMRDYHENVVYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 60
DB      484 KOORRELLFNEVIMRDYHENVVYNSYLVGDELWVMEFEGGALTDIVTHRMNEE 543
QY      61 QIAAVCLAVLOALVLAHQGVHSDIKTD 89
DB      544 QIATVCLSVLRALSYLVHNGVHRIKSD 572

RESULT 3
ID      PAK6 HUMAN
AC      Q9NQ05;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Serine/threonine-protein kinase PAK 6 (EC 2.7.1.-) (p21-activated
DE      kinase 6) (PAK-6) (PAK-5).
GN      PAK6 OR PAK5.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21226785; PubMed=11278661;
RA      Yang F., Li X., Sharma M., Zarnegar M., Lim B., Sun Z.;
RT      "Androgen receptor specifically interacts with a novel p21-activated

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RT      kinase, PAK6.";
RN      J. Biol. Chem. 276:15345-15353(2001).
RL      [2]
RP      SEQUENCE FROM N.A.
RA      Wagner T., Puls A., Frischauf A.M., Hall A.;
RT      "PAK5, a new member of the p21-activated kinase family, affects Cdc42
RT      signalling to the actin cytoskeleton.";
RL      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Caavaant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Young A.C., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -!- FUNCTION: The activated kinase acts on a variety of targets (By
CC      similarity).
CC      -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC      CDC42/P21 AND RAC1 (BY SIMILARITY). INTERACTS WITH THE ANDROGEN
CC      RECEPTOR.
CC      -!- PTM: Autophosphorylated when activated by CDC42/p21 (By
CC      similarity).
CC      -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC      STE20 subfamily.
CC      -!- SIMILARITY: Contains 1 CRIB domain.
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CC      -----
DR      EMBL; AF276893; AAF82800.1; -.
DR      EMBL; AJ236915; AAC18720.1; -.
DR      EMBL; BC035596; AAB35596.1; -.
DR      Genew; HGNC:16061; PAK6.
DR      MIM; 608110; -.
DR      HSSP; P24941; 1A01.
DR      InterPro; IPR000095; PAKbox/RhoDbndng.
DR      InterPro; IPR000719; Prot Kinase.
DR      InterPro; IPR008271; Ser thr pkin AS.
DR      InterPro; IPR002290; Ser thr pkinase.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF00786; PBD; 1.
DR      Pfam; PF00069; pkinase; 1.
DR      PRINTS; PD00109; TYRKINASE.
DR      ProDom; PD000001; Prot Kinase; 1.
DR      SMART; SM00285; PBD; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS50108; CRIB; 1.
DR      PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE NEG.
KW      Transferase; Serine/threonine-protein kinase; ATP-binding;

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KW Phosphorylation.
FT DOMAIN 12 25 CRIB.
FT DOMAIN 26 406 LINKER.
FT DOMAIN 407 658 PROTEIN KINASE.
FT NP_BIND 413 421 ATP (BY SIMILARITY).
FT BINDING 436 436 ATP (BY SIMILARITY).
FT ACT_SITE 526 526 BY SIMILARITY.
SQ SEQUENCE 681 AA; 74868 MW; F20A4FA257649BB9 CRC64;

Query Match 83.8%; Score 379; DB 1; Length 681;
Best Local Similarity 83.1%; Pred. No. 2.5e-31;
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KQORRELFNEVIMRDYHENVVMSYLVGDELWVMEFLGGALTDIVTHRMNEE 60
Db 442 KQORRELFNEVIMRDYHENVVMSYLVGDELWVMEFLGGALTDIVTHRMNEE 501

Qy 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
Db 502 QIATVCEAVLQALVLAHQGVHSDIKTD 530

RESULT 4
PAK1_RAT
ID PAK1_RAT STANDARD; PRT; 544 AA.
AC P35465; Q62934;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated
DE kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK) (protein kinase MUK2).
GN PAK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP Nature 367:40-46(1994).
RC TISSUE=Brain;
RX MEDLINE=94150588; PubMed=8107774;
RA Manser E., Leung T., Salihuddin H., Zhao Z.-S., Lim L.;
RT "A brain serine/threonine protein kinase activated by Cdc42 and
RT Rac1.";
RL Submited (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP Rattus Z.-S.;
RA Zhao Z.-S.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I.,
RA Ohno S.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=96027610; PubMed=7559638;
RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C.,
RA Lim L.;
RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated
RT kinase (PAK) family.";
RL J. Biol. Chem. 270:25070-25078(1995).
CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED
CC GTPASES TO THE JNK MAP KINASE PATHWAY.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1 (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BRAIN, WITH
CC HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH MOTOR
CC FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.
CC -!- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE
CC EXPRESSION ELSEWHERE.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
```

```
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC -----
CC EMBL; U23443; AAB95646.1; -.
CC PDB; U49953; AAB61533.1; -.
CC DR EMBL; U49953; AAB61533.1; -.
CC DR PDB; 1E0A; 14-SEP-00.
CC DR InterPro; IPR000095; PAKbox/RhoBindng.
CC DR InterPro; IPR000719; Prot_Kinase.
CC DR InterPro; IPR008271; Ser_thr_kin_AS.
CC DR InterPro; IPR002290; Ser_thr_kinase.
CC DR InterPro; IPR001245; Tyr_kinase.
CC DR Pfam; PF00786; PBD; 1.
CC DR PRINTS; PR00069; pkinase; 1.
CC DR ProDom; PD000001; Prot_Kinase; 1.
CC DR SMART; SM00285; PBD; 1.
CC DR SMART; SM00220; S_TRK; 1.
CC DR PROSITE; PS010108; CRIB; 1.
CC DR PROSITE; PS010107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS000111; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC DR Transfaser; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation; 3D-structure.
CC FT DOMAIN 75 88 CRIB.
CC FT DOMAIN 89 268 LINKER.
CC FT DOMAIN 269 520 PROTEIN KINASE.
CC FT NP_BIND 275 283 ATP (BY SIMILARITY).
CC FT BINDING 298 298 ATP (BY SIMILARITY).
CC FT ACT_SITE 388 388 BY SIMILARITY.
CC SQ SEQUENCE 544 AA; 60577 MW; 93BE32D822F5B7B CRC64;

Query Match 61.3%; Score 277; DB 1; Length 544;
Best Local Similarity 58.4%; Pred. No. 5.5e-21;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 1 KQORRELFNEVIMRDYHENVVMSYLVGDELWVMEFLGGALTDIVTHRMNEE 60
Db 304 QQPKELIINILVNRKNPNVNYLDSYLVGDELWVMEYLAGSLTDVVTCTMDEG 363

Qy 61 QIAAVCLAVLQALVLAHQGVHSDIKTD 89
Db 364 QIAAVCRECLQALFLHSNQVHSDIKSD 392

RESULT 5
PAK1_HUMAN
ID PAK1_HUMAN STANDARD; PRT; 545 AA.
AC Q13153; Q13567;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.37) (p21-activated
DE kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK).
GN PAK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97199447; PubMed=9395435;
RA Sells M.A., Knaus U.G., Bagrodia S., Ambrose D.M., Bokoch G.M.,
RA Chernoff J.;
RT "Human p21-activated kinase (Pak1) regulates actin organization in
RT mammalian cells.";
```

RL Curr. Biol. 7:202-210(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=96398842; PubMed=8805275;  
 RA Brown J.L., Stowers L., Baer M., Trejo J., Coughlin S., Chant J.;  
 RT "Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinase  
 RL pathway.";  
 RN Curr. Biol. 6:598-605(1996).  
 RP FUNCTION, AND INTERACTION WITH CDC2L1 AND CDC2L2.  
 RX MEDLINE=22651041; PubMed=12624090;  
 RA Chen S., Yin X., Zhu X., Yan J., Ji S., Chen C., Cai M., Zhang S.,  
 Zong H., Hu Y., Yuan Z., Shen Z., Gu J.;  
 RT "The C-terminal kinase domain of the p34cdc2-related PITSURE protein  
 RT kinase (p110C) associates with p21-activated kinase 1 and inhibits  
 RT its activity during anokis.";  
 RL J. Biol. Chem. 278:20029-20036(2003).  
 CC -!- FUNCTION: The activated kinase acts on a variety of targets.  
 CC Likely to be the GTPase effector that links the Rho-related  
 CC GTPases to the JNK MAP kinase pathway. Activity inhibited in cells  
 CC undergoing apoptosis, potentially due to binding of CDC2L1 and  
 CC CDC2L2.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- COFACTOR: Magnesium.  
 CC -!- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound  
 CC CDC42/p21 and RAC1. Binds to the caspase-cleaved p110 isoform of  
 CC CDC2L1 and CDC2L2, p110C, but not the full-length proteins.  
 CC -!- PTM: Autophosphorylated when activated by CDC42/p21.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC STE20 subfamily.  
 CC -!- SIMILARITY: Contains 1 CRIB domain.  
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 CC -----  
 DR EMBL; U24152; AAA65441.1; -;  
 DR EMBL; U51120; AAC50590.1; -;  
 DR PIR; G01773; G01773.  
 DR PDB; 1E3M; 29-NOV-00.  
 DR Genew; HGNC:8590; PAK1.  
 DR MIM; 602590; -;  
 DR GO; GO:0007254; P:JNK cascade; TAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
 DR InterPro; IPR000095; PAKbox/RhoBndng.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00220; S\_TKG; 1.  
 DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Apoptosis; Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 RX Phosphorylation; 3D-structure.  
 FT DOMAIN 75 88 CRIB.  
 FT 89 269 LINKER.  
 FT DOMAIN 270 521 PROTEIN\_KINASE.  
 FT NP\_BIND 276 284 ATP (BY SIMILARITY).  
 FT BINDING 299 299 ATP (BY SIMILARITY).  
 FT ACT\_SITE 389 389 BY SIMILARITY.  
 FT MUTAGEN 107 107 L->F: CONSTITUTIVELY ACTIVE.

FT CONFLICT 26 26 V -> A (IN REF. 2).  
 FT CONFLICT 237 237 R -> L (IN REF. 2).  
 FT CONFLICT 379 379 F -> S (IN REF. 2).  
 FT CONFLICT 503 503 D -> E (IN REF. 2).  
 SQ SEQUENCE 545 AA; 60661 MW; 14A1E70B6480CD7E CRC64;  
 Query Match 61.3%; Score 277; DB 1; Length 545;  
 Best Local Similarity 58.4%; Pred No. 5.6e-21;  
 Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 KQORRELLFNEVIMRDYRHENVEMYSYLVGDELWVMEFEGGALFDIVYTHRMNEE 60  
 Db 305 QQPKKELINEILVMKNPNVLYDSYLVGDELWVMEYLAGSLTDVVTETCMDSG 364  
 QY 61 QTAACVLAQLQALAVLHAQGVHSDIKTD 89  
 Db 365 QTAACVRECLQALEFLHSNQVHRIKSD 393  
 RESULT 6  
 PAK1 MOUSE  
 ID PAK1 MOUSE STANDARD; PRT; 545 AA.  
 AC O88643;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated  
 DE kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK) (CDC42/RAC effector kinase  
 DE PAK-A).  
 GN PAK1 OR PAKA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99282526; PubMed=10352232;  
 RA Burdello P.D., Korak C.A., Finegold A.A., Hall A., Pirone D.M.;  
 RT "Cloning, central nervous system expression and chromosomal mapping of  
 RT the mouse PAK-1 and PAK-3 genes.";  
 RL Gene 232:209-215(1999).  
 CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
 CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED  
 CC GTPASES TO THE JNK MAP KINASE PATHWAY (BY SIMILARITY).  
 CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
 CC CDC42/p21 AND RAC1 (BY SIMILARITY).  
 CC -!- PTM: Autophosphorylated when activated by CDC42/p21 (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC STE20 subfamily.  
 CC -!- SIMILARITY: Contains 1 CRIB domain.  
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 CC -----  
 DR EMBL; AF082077; AAC32375.1; -;  
 DR HSSP; P24941; 1CKP.  
 DR MGD; MGT133975; PAK1.  
 DR GO; GO:0005737; Cytoplasm; IDA.  
 DR GO; GO:0016358; P:denitrification morphogenesis; IDA.  
 DR InterPro; IPR000095; PAKbox/RhoBndng.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.

```

DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0285; PBD; 1.
DR MIM; 300142; -.
DR InterPro; IPR000095; PAKbox/RhoBindng.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 75 88 CRIB
FT DOMAIN 89 267 LINKER.
FT DOMAIN 270 521 PROTEIN_KINASE.
FT NP_BIND 276 284 ATP (BY SIMILARITY).
FT BINDING 299 299 ATP (BY SIMILARITY).
FT ACT_SITE 389 389 BY SIMILARITY.
SQ SEQUENCE 545 AA; 60737 MW; A4861289534C3819 CRC64;

Query Match 61.3%; Score 277; DB 1; Length 545;
Best Local Similarity 58.4%; Pred. No. 5.6e-21;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHNENVMNSYLVGDELWVMEFLEGALTDIVTHRMNEE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 305 QQPKKELLINEILVMRENKNFNIVNLDYLVGDELWVMEYLAGSLTDVVTEICMDEG 364

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDKTD 89
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 365 QIAAVCRECLQALEFLHSNQVTHRIDKSD 393

RESULT 7
PAK3 HUMAN
ID PAK3 HUMAN STANDARD; PRT; 544 AA.
AC O75914;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
DE kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3).
GN PAK3 OR OPHN3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND DISEASE.
RX MEDLINE=98400251; PubMed=9731525;
RA Allen K.M., Gleeson J.G., Bagrodia S., Partington M.W.,
RA Macmillan J.C., Cerione R.A., Mulley J.C., Walsh C.A.;
RA "PAK3 mutation in nonsyndromic X-linked mental retardation.";
RL Nat. Genet. 20:25-30(1998).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN POSTMITOTIC NEURONS OF THE
CC DEVELOPING AND POSTNATAL CEREBRAL CORTEX AND HIPPOCAMPUS.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- DISEASE: Defects in PAK3 are the cause of non-specific X-linked
CC nonsyndromic mental retardation type 30 (MRX30) [MIM:300142].
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC ST220 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC -----
DR EMBL; AF068864; AAC36097.1; -.

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CC -1- PTM: Autophosphorylated when activated by CDC42/p21.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC STE20 subfamily.  
 CC -1- SIMILARITY: Contains 1 CRIB domain.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: U33314; AAC52268.1; -;  
 DR PIR: A57597; A57597.  
 DR HSSP: P24941; 1CKP.  
 DR InterPro: IPR000095; PAKbox/RhoGndg.  
 DR InterPro: IPR000719; Protein kinase.  
 DR InterPro: IPR008271; Ser Thr\_pkin AS.  
 DR InterPro: IPR002290; Ser Thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00786; PBD; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PD00109; TYRKINASE.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_TK; 1.  
 DR PROSITE: PS50108; CRIB; 1.  
 DR PROSITE: PS50107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 70 83 CRIB.  
 FT DOMAIN 84 267 LINKER.  
 FT DOMAIN 268 519 PROTEIN\_KINASE.  
 FT NP\_BIND 274 282 ATP (BY SIMILARITY).  
 FT BINDING 297 297 ATP (BY SIMILARITY).  
 FT ACT\_SITE 387 387 BY SIMILARITY.  
 SQ SEQUENCE 544 AA; 60710 MW; 7B940FC204A2B48B CRC64;  
 Query Match 61.1%; Score 276; DB 1; Length 544;  
 Best Local Similarity 58.4%; Pred. No. 7e-21;  
 Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 KQORRELLNEVIMRDYRHENVVMSYLVGDELWVMEFLGCGALTDIVTHRMNEE 60  
 Db 303 QQPKKELIINEILVMENKNPNIVYLDYSLVGDLEWVMEYLAGGSLTDVVTTCMDEG 362  
 QY 61 QIAAVCLAVLQALVLAHQGVHSIDKTD 89  
 Db 363 QIAAVCREGLQALDFLHNSQVIRDIKSD 391  
 RESULT 9  
 ID PAK2 HUMAN STANDARD; PRT; 524 AA.  
 AC Q13177; Q13154;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated  
 DE kinase 2) (PAK-2) (PAK65) (Gamma-PAK) (S6/H4 kinase).  
 GN PAK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Sells M., Knause U.J., Bagrodia S., Ambrose D., Bokoch G.M.,  
 RA Chernoff J.,  
 Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE OF 32-524 FROM N.A., AND SEQUENCE OF 401-417.  
 RC TISSUE=Placenta;  
 RX MEDLINE=95262637; PubMed=7744004;  
 RA Martin G.A., Bollag G., McCormick F., Abo A.;  
 RT "A novel serine kinase activated by rac1/CDC42Hs-dependent  
 RT autophosphorylation is related to PAK65 and STE20.";  
 RL EMBO J. 14:1970-1978(1995).  
 CC [3]  
 RN ERRATUM.  
 RP MEDLINE=96016211; PubMed=7556080;  
 RX Martin G.A., Bollag G., McCormick F., Abo A.;  
 RA EMBO J. 14:4385-4385(1995).  
 CC [4]  
 RN AUTOPHOSPHORYLATION.  
 RP MEDLINE=95403344; PubMed=7673144;  
 RX Benner G.E., Dennis P.B., Masaracchia R.A.;  
 RT "Activation of an S6/H4 kinase (PAK 65) from human placenta by  
 RT intramolecular and intermolecular autophosphorylation.";  
 RL J. Biol. Chem. 270:21121-21128(1995).  
 CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
 CC PHOSPHORYLATES RIBOSOMAL PROTEIN S6, HISTONE H4 AND MYELIN BASIC  
 CC PROTEIN.  
 CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
 CC CDC42/p21 AND RAC1.  
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. HIGHER LEVELS SEEN IN  
 CC SKELETAL MUSCLE, OVARY, THYMUS AND SPLEEN.  
 CC -1- PTM: Autophosphorylated when activated by CDC42/p21.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC STE20 subfamily.  
 CC -1- SIMILARITY: Contains 1 CRIB domain.  
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 CC EMBL: U24153; AAA65442.1; -;  
 DR EMBL: U25975; AAA75468.1; -;  
 DR PIR: S58682; S58682.  
 DR HSSP: P24941; 1CKP.  
 DR Genew: HGNC:8591; PAK2.  
 DR MIM: 605022; -;  
 DR GO: GO:0004672; F:protein kinase activity; TAS.  
 DR GO: GO:0006469; P:negative regulation of protein kinase activity; TAS.  
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.  
 DR GO: GO:0007165; P:signal transduction; TAS.  
 DR InterPro: IPR000095; PAKbox/RhoGndg.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR008271; Ser Thr\_pkin AS.  
 DR InterPro: IPR002290; Ser Thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00786; PBD; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PD00109; TYRKINASE.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_TK; 1.  
 DR PROSITE: PS50108; CRIB; 1.  
 DR PROSITE: PS50107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 74 87 CRIB.  
 FT DOMAIN 88 248 LINKER.  
 FT DOMAIN 249 499 PROTEIN\_KINASE.  
 FT NP\_BIND 255 263 ATP (BY SIMILARITY).  
 FT BINDING 278 278 ATP (BY SIMILARITY).  
 FT ACT\_SITE 367 367 BY SIMILARITY.

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FT CONFLICT 90 A -> T (IN REF. 2).
FT CONFLICT 150 L -> P (IN REF. 2).
FT CONFLICT 225 P -> T (IN REF. 2).
FT CONFLICT 329 G -> R (IN REF. 2).
FT CONFLICT 338 T -> TA (IN REF. 1).
SQ SEQUENCE 524 AA; 58004 MW; DB2A7A72BE6B1072 CRC64;

Query Match
Best Local Similarity 60.6%; Score 274; DB 1; Length 524;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYSYLVGDELWVMEFLGGLTIDIVTHTRMNEE 60
Db 284 KQPKKELIINEILVMKELKNPNVNFVLDYLVGDELWVMEFLGGLTIDIVTHTRMNEE 60
QY 61 QIAAVCLAVLOALVILHAQGVHSDIKTD 89
Db 344 QIAAVCRECLQALEFLHANQVHRIKSD 372

RESULT 10
ID PAK2 RABIT STANDARD; PRT; 524 AA.
AC Q29502;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated
DE kinase 2) (PAK-2) (Gamma-PAK) (p21-activated protein kinase 1)
DE (PAK1).
GN PAK2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198078; PubMed=8626411;
RA Jakobi R., Chen C., Tuazon P.T., Traugh J.A.;
RT "Molecular cloning and sequencing of the cytosolic G protein-
RT activated protein kinase PAK 1."
RL J. Biol. Chem. 271:6206-6211(1996).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/p21 AND RAC1.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC -----
CC EMBL; U46915; AAC48537.1; --
CC HSSP; P24941; 1CKP.
CC -----
CC InterPro; IPR000095; PAKbox/RhoGndng.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00786; PBD; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00285; PBD; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00108; CRIB; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
```

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DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 74 87 CRIB.
FT DOMAIN 88 248 LINKER.
FT DOMAIN 249 500 PROTEIN_KINASE.
FT NP_BIND 255 263 ATP (BY SIMILARITY).
FT BINDING 278 278 ATP (BY SIMILARITY).
FT ACT_SITE 368 368 BY SIMILARITY.
SQ SEQUENCE 524 AA; 58027 MW; 39D71020EADFFCA CRC64;

Query Match
Best Local Similarity 60.6%; Score 274; DB 1; Length 524;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYSYLVGDELWVMEFLGGLTIDIVTHTRMNEE 60
Db 284 KQPKKELIINEILVMKELKNPNVNFVLDYLVGDELWVMEFLGGLTIDIVTHTRMNEE 60
QY 61 QIAAVCLAVLOALVILHAQGVHSDIKTD 89
Db 344 QIAAVCRECLQALEFLHANQVHRIKSD 372

RESULT 11
ID PAK2 RAT STANDARD; PRT; 524 AA.
AC Q64303;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated
DE kinase 2) (PAK-2) (Gamma-PAK) (P62-PAK).
GN PAK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Brain, and Testis;
RX MEDLINE=96064759; PubMed=7592896;
RA Teo M., Manser E., Lim L.;
RT "Identification and molecular cloning of a p21cdc42/rac1-activated
RT serine/threonine kinase that is rapidly activated by thrombin in
RT platelets".
RL J. Biol. Chem. 270:26690-26697(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Mabel T.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/p21 AND RAC1.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S80221; AAB35608.1; --
CC EMBL; U35345; AAA79064.1; --
CC HSSP; P24941; 1CKP.
CC InterPro; IPR000095; PAKbox/RhoGndng.
```

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DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 74 87 CRIB.
FT DOMAIN 88 248 LINKER.
FT DOMAIN 249 500 PROTEIN_KINASE.
FT NP_BIND 255 263 ATP (BY SIMILARITY).
FT BINDING 278 278 ATP (BY SIMILARITY).
FT ACT_SITE 368 368 BY SIMILARITY.
SQ SEQUENCE 524 AA; 57960 MW; A3F2FE81C8D4294 CRC64;

Query Match 60.6%; Score 274; DB 1; Length 524;
Best Local Similarity 58.4%; Pred. No. 1.1e-20;
Matches 52; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVVMSYLVGDELWVMEFLGGLTIDVTHTRMNEE 60
DB 284 KQPKKELINEILVMKELNPNVFLSYLVGDELWVMEFLGGLTIDVTHTRMNEE 60
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 344 QIAAVCRECLQALFELHANQVHRIKSD 372

RESULT 12
PAK3 MOUSE
ID_PAK3_MOUSE STANDARD; PRT; 544 AA.
AC Q61036; O88645;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
DE kinase 3) (PAK-3) (Beta-PAK) (CDC42/RAC effector kinase PAK-B).
GN PAK3 OR PAK-3 OR STK4 OR PAKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
(1)
RN SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=96032893; PubMed=7559398;
RA Bagrodia S., Taylor S.J., Creasy C.L., Chernoff J., Cerione R.A.;
RT "Identification of a mouse p21cdc42/Rac activated kinase.";
RL J. Biol. Chem. 270:22731-22737(1995).
(2)
RN SEQUENCE FROM N.A.
RP ERRATUM.
RA Bagrodia S., Taylor S.J., Creasy C.L., Chernoff J., Cerione R.A.;
RL J. Biol. Chem. 271:1250-1250(1996).
(3)
RN SEQUENCE FROM N.A.
RX MEDLINE=99282526; PubMed=10352232;
RA Burdello P.D., Kozak C.A., Finegold A.A., Hall A., Pirone D.M.;
RT "Cloning, central nervous system expression and chromosomal mapping of
RT the mouse PAK-1 and PAK-3 genes.";
RL Gene 232:209-215(1999).
CC -!- FUNCTION: The activated kinase acts on a variety of targets.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
```

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CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U39738; AAC52354.1; -
CC EMBL; AF082297; AAC31969.1; -
CC PIR; I49376; I49376.
CC PDB; 1EES; 12-APR-00.
CC MGD; MGI:1339656; Pak3.
CC InterPro; IPR000095; PAKbox/RhoGndng.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00786; PBD; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00285; PBD; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00108; CRIB; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW SH3-binding; Phosphorylation; 3D-structure.
FT DOMAIN 70 83 CRIB.
FT DOMAIN 84 267 LINKER.
FT DOMAIN 268 519 PROTEIN_KINASE.
FT NP_BIND 274 282 ATP (BY SIMILARITY).
FT BINDING 297 297 ATP (BY SIMILARITY).
FT ACT_SITE 387 387 BY SIMILARITY.
FT CONFLICT 161 161 G -> A (IN REF. 3).
FT CONFLICT 361 361 V -> E (IN REF. 3).
FT CONFLICT 493 493 H -> R (IN REF. 3).
FT CONFLICT 525 525 L -> M (IN REF. 3).
SQ SEQUENCE 544 AA; 60693 MW; C4AEB7LDD33E6988 CRC64;

Query Match 59.5%; Score 269; DB 1; Length 544;
Best Local Similarity 57.3%; Pred. No. 3.7e-20;
Matches 51; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENVVMSYLVGDELWVMEFLGGLTIDVTHTRMNEE 60
DB 303 QQPKKELINEILVMKELNPNVFLSYLVGDELWVMEFLGGLTIDVTHTRMNEE 60
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 363 QIAAVCRECLQALFELHANQVHRIKSD 391

RESULT 13
STE20 CANAL
ID_STE20_CANAL STANDARD; PRT; 1230 AA.
AC Q92212;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase STE20 homolog (EC 2.7.1.-).
GN HSR20 OR GST20.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1066;
RX  MEDLINE=97075146; PubMed=8917572;
RA  Kohler J.R., Fink G.R.;
RT  "Candida albicans strains heterozygous and homozygous for mutations
RT  in mitogen-activated protein kinase signaling components have defects
RT  in hyphal development.";
RL  Proc. Natl. Acad. Sci. U.S.A. 93:13223-13228(1996).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC  STE20 subfamily.
CC  -!- SIMILARITY: Contains 1 CRIB domain.
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  EMBL; U73457; AAB38875.1; -.
DR  PIR; T18259; T18259.
DR  HSSP; Q63450; 1A06.
DR  InterPro; IPR000095; PAKbox/RhoGndng.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  Pfam; PF00786; PKB; 1.
DR  Pfam; PF00069; pkinase; 1.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00285; PBD; 1.
DR  SMART; SM00220; S_TK; 1.
DR  PROSITE; PS0108; CRIB; 1.
DR  PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  Transferase; Serine/threonine-protein kinase; ATP-binding.
FT  DOMAIN 109 119 POLY-ASN.
FT  DOMAIN 290 293 POLY-PRO.
FT  DOMAIN 453 464 POLY-SER.
FT  DOMAIN 552 555 POLY-SER.
FT  DOMAIN 573 580 POLY-GLY.
FT  DOMAIN 727 732 POLY-PRO.
FT  DOMAIN 790 794 POLY-PRO.
FT  DOMAIN 475 488 CRIB.
FT  DOMAIN 953 1205 PROTEIN_KINASE.
FT  NP_BIND 959 967 ATP (BY SIMILARITY).
FT  BINDING 983 983 ATP (BY SIMILARITY).
FT  ACT_SITE 1073 1073 BY SIMILARITY.
SQ  SEQUENCE 1230 AA; 132862 MW; 2B2AC4C133B9FE81 CRC64;

Query Match          56.6%; Score 256; DB 1; Length 1230;
Best Local Similarity 50.6%; Pred. No. 1.8e-18;
Matches 45; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY  1 KQORRELFNEVIVRDYTHENVEMNSYLVGDELWVMEFEGGALTDIVYTHRMNEE 60
DB  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  989 QQPKKELINEILVMKGSHPNINFDISLLKGLWIMETMEGSLTDIVYTHSVMTG 1048
QY  61 QIAAVCLAVLOALVLAHAGVTHSDIKD 89
DB  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  1049 QIGVVCRETLLKGLKFLHSGVHHRDKSD 1077

RESULT 14
ST20 YEAST
ID ST20_YEAST STANDARD; PRT; 939 AA.
AC Q03457;
DT 01-OCT-1993 (Rel. 27, Created)
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DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Pheromone response; Phosphorylation.
FT DOMAIN 337 350 CRIB.
FT DOMAIN 620 871 PROTEIN_KINASE.
FT NP_BIND 626 634 ATP (BY SIMILARITY).
FT BINDING 649 649 ATP (BY SIMILARITY).
FT ACT_SITE 739 739 BY SIMILARITY.
FT CONFLICT 19 19 N -> S (IN REF. 2).
FT CONFLICT 134 134 I -> M (IN REF. 2).
FT CONFLICT 271 271 P -> S (IN REF. 2).
SQ SEQUENCE 939 AA; 102362 MW; 69C1C12F5B87733C CRC64;

Query Match 56.4%; Score 255; DB 1; Length 939;
Best Local Similarity 48.3%; Pred. No. 1.8e-18;
Matches 43; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVIMRDYRHENVVMYNSYLVGDELVVMVEFEGGALTDIVTHRMNEE 60
DB 655 KQPKELIINEILVMKSGKPNVFNFDYSLVGLWIMVMEGSLTDVVTCHILLEG 714

QY 61 QIAAVCLAVLQALVLAHAGVHSDIKTD 89
DB 715 QIGAVCRETSLGLEFLHSGKGLVRDIKSD 743

RESULT 15
CLA4 CANAL STANDARD; PRT; 971 AA.
AC O14427;
AT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase CLA4 (EC 2.7.1.-).
GN CLA4.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97411146; PubMed=9259554;
RA Leberer E., Ziegelbauer K., Schmidt A., Marcus D., Dignard D., Ash J.,
RA Johnson L., Thomas D.Y.
RT "Virulence and hyphal formation of Candida albicans require the
RT Ste20p-like protein kinase CaCl4p."
RL Curr. Biol. 7:539-546(1997).
RC -!- FUNCTION: Essential for virulence and morphological switching
CC (hyphal formation) of C.albicans.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
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CC -----
DR EMBL; U87396; AAB68613.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000095; PAKbox/RhoBindng.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS0003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 67 178 PH.
FT DOMAIN 231 244 CRIB.
FT DOMAIN 680 935 PROTEIN_KINASE.
FT DOMAIN 16 19 POLY-PRO.
FT DOMAIN 210 213 POLY-SER.
FT DOMAIN 311 315 POLY-ASN.
FT DOMAIN 384 389 POLY-ASN.
FT DOMAIN 392 395 POLY-ASN.
FT DOMAIN 418 421 POLY-PRO.
FT DOMAIN 453 462 POLY-GLN.
FT DOMAIN 468 476 POLY-GLN.
FT DOMAIN 572 576 POLY-GLN.
FT NP_BIND 686 694 ATP (BY SIMILARITY).
FT BINDING 710 710 ATP (BY SIMILARITY).
FT ACT_SITE 803 803 BY SIMILARITY.
SQ SEQUENCE 971 AA; 106889 MW; AD6F0DBBC6CF624B CRC64;

Query Match 55.0%; Score 248.5; DB 1; Length 971;
Best Local Similarity 47.3%; Pred. No. 8.5e-18;
Matches 43; Conservative 27; Mismatches 18; Indels 3; Gaps 2;

QY 2 QORRELLFNEVIMRDYRHENVVMYNSYLVGDELVVMVEFEGGALTDIVTHRMNEE 58
DB 717 QPKELIINEILVMKDSQHKINFLDLSYLGDNELWIMVMEYMQGSLTEIENNDFKIN 776

QY 59 EEQIAAVCLAVLQALVLAHAGVHSDIKTD 89
DB 777 EQIATICFETLKGLOLHUKKHHRDIKSD 807

Search completed: September 29, 2004, 18:02:01
Job time : 2.48676 secs

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